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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Prostate-specific membrane transmembrane glycoprotein; antibody detection; ds.
                                                                                                                                                                                                  Claim
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PA (CTLI-) CTL IMMUNOTHERAPIES CORP.

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PI Simard JJL, Diamond DC;

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PP Simard JJL, Diamond DC;

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WPI; 2002-750433/81.

DR p-PSDB; ABG98045.

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Evaluating cell-mediated immunity, in particular cytotoxic T lymphocyte responses, by implanting vascular cells, useful for treatment and presearch models for directly targeting tumor neovasculature - xx

Evaluating cell-mediated immunity comprising implanting vascular cells into an immunodeficient mammal. CC comprising implanting vascular cells into an immunodeficient mammal. CC establishing an immune response in the mammal, and assaying a characteristic to determine cell-mediated immunity in the mammal. The CC comprising an immune response in the mammal, and assaying a comprising an immune response in the mammal invention are useful for the CC continued and compositions of the present invention are useful for the cc used for making research models targeting tumour neovasculature. They can also be continued growth. This approach at targeting tumour neovasculature. They can also be continued growth. This approach alms to disrupt to support their continued growth. This approach alms to disrupt a tumour's supply of nutrients to cause it to die or at least limit its growth. This sequence crepresents a DNA associated with the neo-vascularature preparation for treatment of cancer desciribed in the invention.
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Sequence Similarity 2653 BP; Conservative 782 98.5%; Α, 524 C; 0; Score 1702.6; Pred. No. 0; Mismatches 640 G; 707 Τ; DB 24; 0 other; 24; Length Indels 2653; 2; Gaps

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response against a cell comprising a target antigen (I) in a subject, cureating a subject having undesired cells, for example tumour cells or virally infected cells (C), reducing the number of (C) in a subject, and stimulating presentation of (I) by a cell. This is done by a diministering a polynucleotide (II) encoding a variant of (I), so that (II) expressed in a cell and cell-mediated immune response is induced. The method can be used to treat prostate cancer, breast cancer, colorectal cancer and pancreatic cancer, as well as lymphomas and leukaemias. The method is also useful in treating chronic viral infections such as those caused by hepadnaviruses, lentiviruses and the flaviviruses and pestiviruses. The present sequence represents the coding sequence of human prostate specific membrane antigen (PSMA) variant which has the signal sequence deleted, used as a target antigen in the
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                                                                                               TTTATGAAAGTTGGACTAAAAAAAAGTCCTTCCCCAGAGTTCAGTGGCATGCCCAGGATAA
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LD ABK64556 standard; DNA; 2653 BI
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ABK64556;

18-JUN-2002 (first entry)
Human benign prostatic hyp
Human; benign prostatic hy
Homo sapiens.

hyperplasia g c hyperplasia;

gene #451 a; BPH; pro

prostate

cancer;

gene; ds

WO200212440-A2 14-FEB-2002.

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Matches 1729
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h; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
atic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
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                                                                                                           CC anti-neoplastic agent. The method involves exposing cells to a chemical Ca agent to be tested for anti-neoplastic activity, determining a change in CC expression of at least one gene (I) of a signature gene set, where (I) CC comprises a sequence (S) selected from 8447 sequences (given in ABL61664 CC to ABL70110), or is at least 95% identical to (S), where a change in CC expression is indicative of anti-neoplastic activity. (I) has cytostatic CC activity and can be used in gene therapy. MI can be used for screening CC an anti-neoplastic agent, and can be used for producing a product which CC is the data collected with respect to the anti-neoplastic agent as a CC result of MI, and the data is sufficient to convey the chemical CC treatment of cancer such as colon, breast, stomach, lung, thyroid, CC oesophageal, ovarian, kidney, prostate or pancreatic cancer, adenocarcinoma, carcinoma, clear cell carcinoma, neuroendocrine CC carcinoma, carcinoma, clear cell carcinoma, neuroendocrine CC carcinoma, acadilary carcinoma and wilm's tumour
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Sequence 2653 BP; 782 A; 524 C; 640 G; 707 T; 0 other;

papillary carcinoma

and Wilm's tumour.

Query Match Best Local

Similarity

98.5%;

Score 1702.6;

DB 24;

Length

2653;

δÃ δÃ B Ş B Ş В ΔÃ Matches 1729; 1079 1019 480 420 959 300 240 TCCAGCGTGGAAATATCCTAAATCTGAATGGTGCAGGAGACCCTCTCACACCAGGTTACC ACTACTTTGCTCCTGGGGTGAAGTCCTATCCAGACGGTTGGAATCTTCCTGGAGGTGGTG AGGTTAAAAATGCCCAGCTGGCAGGGGCCAAAGGAGTCATTCTCTACTCAGACCCTGCTG CAGCAAATGAATACGCTTATAGGCATGGAAATTGCAGAGGCTGTTGGTCTTCCAAGTATTC CAGCAAATGAATATGCTTATAGGCGTGGAATTGCAGAGGCTGTTGGTCTTCCAAGTATTC AGGTTAAAAATGCCCAGCTGGCAGGGGCCAAAGGAGTCATTCTCTACTCCGACCCTGCTG Conservative 0; Pred. No. 0; 0; Mismatches 24; Indels 2; Gaps 1078 1018 1198 539 1138 419 359 958 299

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25-MAY-2000;
09-JUN-2000;
18-JUL-2000;
13-DEC-2000;
                                                                                                                                                                                                                                                                                                                                           a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of t specification or its complement. (I) is useful for:
(a) assessing whether a patient is afflicted with prostate cancer;
(b) monitoring the progression of prostate cancer in a patient;
(c) assessing the efficacy of a test compound to inhibit prostate cancer in a patient;
                                                                                                                                                                                                                                                                                        (a) ass
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16-MAR-2000;
25-MAY-2000;
09-JUN-2000;
18-JUL-2000;
13-DEC-2000;
The invention relates to an isolated nucleic acid molecule (I) a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) c specification or its complement. (I) is useful for:
(a) assessing whether a patient is afflicted with prostate cancel (b) monitoring the progression of prostate cancer in a patient.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; prostate pharmacogenomic
                                                                                                                    Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer, stage of prostate cancer.
                                                                                            Claim
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(I) is also useful as
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selecting a composition for inhibiting prostate cancer in a assessing the prostate cell carcinogenic potential of a comp determining whether prostate cancer has metastasized in a pa assessing the aggressiveness or indolence of prostate cancer of a compound;
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a pharmacodyanamic or pharmacogenomic marker

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Score 1702.6; Pred. No. 0; 0; Mismatches DB 24; 23; Indels Length 2; Gaps

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TTCTGGGAGGTCACCGGGACTCATGGGTGTTTGGTGGTATTGACCCTCAGAGTGGAGCAG TTCTGGGAGGTCACCGGGACTCATGGGTGTTTGGTGGTATTGACCCTCAGAGTGGAGCAG

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Novel isolated prostate cells for detecting p presence nucleic acid molecule associated with cancerous state of and correlating with presence of prostate cancer, useful presence of prostate cancer -

a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) c specification or its complement. (I) is useful for:
(a) assessing whether a patient is afflicted with prostate cance (b) monitoring the progression of prostate cancer in a patient;
(c) assessing the efficacy of a test compound to inhibit prostat (d) assessing the efficacy of a test compound in a patient;
(c) assessing the efficacy of a theorem. selecting a composition for inhibiting prostate cancer i assessing the prostate cell carcinogenic potential of a determining whether prostate cancer has metastasized in assessing the aggressiveness or indolence of prostate can also useful as a pharmacodyanamic or pharmacogenomic in a patient; cancer in a r in a patient; a compound; in a patient; cancer; marker

2884 BP; 851 Α; 551 Ç 684 ç; 784 T; 14 other;

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AGGTTAAAAATGCCCAGCTGGCAGGGGCCAAAGGAGTCATTCTCTACTCAGACCCTGCTG CAGCAAATGAATACGCTTATAGGCATGGAATTGCAGAGGCTGTTGGTCTTCCAAGTATTC ACTACTTTGCTCCTGGGGTGAAGTCCTATCCAGACGGTTGGAATCTTCCTGGAGGTGGTG CAGCAAATGAATATGCTTATAGGCGTGGAATTGCAGAGGCTGTTGGTCTTCCAAGTATTC Conservative 0; Score 1702.6; Pred. No. 0; 0; Mismatches 24; Gaps 1262 1202 1142 539 479 419 359

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The invention relates to an isolated nucleic acid molecule a nucleotide sequence given in Tables 1-9 (ABV00010-ABV6221: specification or its complement. (I) is useful for: (a) assessing whether a patient is afflicted with prostate

prostate cancer;

) comprising of the

Claim

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Novel isolated nucleic acid molecule associated with cancerous s: prostate cells and correlating with presence of prostate cancer, for detecting presence of prostate cancer, stage of prostate can

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                                                             AGTGGGCAGAGGATAATTCAAGACTCCTTCAAGAGCGTGGCGTGGCTTATATATTGATGCTG
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                                                                                                                                                      A cDNA clone (AAT36785) codes for human 100 kDa prostate-specific membrane (PSM) antigen (AAW02234), an integral membrane glycoprotein that is very highly expressed in prostatic tumours and metastases. It was obtd. from lymph node carcinoma of prostate (LNCaP) cell mRNA by PCR amplification (see also AAT36795-808) and screening of ar LNCaP cDNA library using an amplified cDNA partial clone as probe The cDNA can be used to provide probes and primers useful e.g. in detecting hematogenous micrometastatic tumour cells and determining prostate cancer progression (see also AAT36827-30 and AAT36813-18), and in gene therapy. An alternatively spliced PSM, PSM', has a shorter cDNA sequence. PSM genomic DNA is given in AAT36786.
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06-JAN-2000;
06-JAN-2000;
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Ferrara N,
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Novel PRO polypeptides and polynucleotides used to target bioactive molecules to specific cells, cellular activities -
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; 2000WO-US00277.
; 2000WO-US00376.
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Desnoyers L, Eaton I

Desnoyers L, Eaton I

Gurney AL, Hillan I

J, Paoni NF, Roy MA,

Illiams PM, Wood WI;
                    in detection, and to modul
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Gerritsen
                    ction methods, modulate
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Sequence 2558 BP; 745 A; 509 C; 623 G; 681 T; 0 other;

84.7%; Score 1687.2; Pred. No. 0; 0; Mismatches 0; ₽B 23; 21; Indels Length 2 Gaps

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TTACTGGAAACTTTTCTACACAAAAAGTCAAGATGCACATCCACTCTACCAATGAAGTGA
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                                             CAGCAAATGAATACGCTTATAGGCATGGAATTGCAGAGGCTGTTGGTCTTCCAAGTATTC
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CTCCAAGCAGCCACAACAAGTATGCAGGGGAGTCATTCCCAGGAATTTATGATGCTCTGT
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2000US-196687P
2000US-196680P
2000US-19682PP
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2000US-19654P
2000WO-US14941
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2000WO-US15264
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2000WO-US13232B
2000WO-US2332B
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Human DNA encoding
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         (first
PRO
                            cDNA;
        entry)
polypeptide
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sequence
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PRO polypeptide; mammal; tumour; cancer; human; cattle; horse; sheep; ss; dog; cat; pig; goat; rabbit; tumour necrosis factor alpha; TNF-alpha; blood; chondrocyte cell; cell proliferation; cell differentiation; colon; adrenal; lung; breast; prostate; rectum; cervix; liver; genetic disorder;

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CC can be used for genetic analysis of individuals with genetic disorders.
                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
Matches 1713; Conserv
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  of tumours, such as prostate and breast tumours, in mammals and
n for modulators of the compounds -
                                           TTACTGGAAACTTTTCTACACAAAAAGTCAAGATGCACATCCACTCTACCAATGAAGTGA
                                                                                                                                   CACCACCAGATAGCAGCTGGAGAGGAAGTCTCAAAGTGTCCTACAATGTTGGACCTGGCT
                                                                                                                                                                              CTGTTCATCCAGTTGGATACTATGATGCACAGAAGCTCCTAGAAAAAATGGGTGGCTCAG
                                                                                                                                                                                                                           TTCTGGGAGGTCACCGGGACTCATGGGTGTTTGGTGGTATTGACCCTCAGAGTGGAGCAG
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98.6%;
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                                                                                                                                                                                           TTGACAAAAGCAACCCAATAGTATTAAGAATGATGATGATCAACTCATGTTTCTGGAAA
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07-CCT-1998;
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24-FEB-2000;
27-MAR-2000;
28-JUN-2000;
29-JUN-2000;
20-JUN-2000;
21-MAR-2000;
21-MAR-2000;
22-MAY-2000;
23-MAY-2000;
24-AUG-2000;
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tumour necrosis
differentiation;
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98WO-US25108
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97US-063374P.
97US-063734P.
97US-06370P.
97US-066110P.
97US-066120P.
98US-07632P.
98US-07632P.
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ALIGNMENTS

	MEDLINE-98362085; PubMed-9694964; Luthi-Carter R., Barczak A.K., Speno H., Coyle J.T.;	RX A
	SEQUENCE FROM N.A. (ISOFORM PSMA-1). TISSUE-Brain;	R R
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	prostate-specific membrane antigen gene."; Biochim. Biophys. Acta 1443:113-127(1998).	2 Y
	organization and	RT
	r R.A., Fair W.R., Heston W.D.W.;	RA
	Zandvliet D., Russell P.J., Molloy P.L., Nowak N.J., Shows T.B.,	RA A
	Bacich D.T. Borignohi v Tho v Dowell C.T.	Z X
	SEQUENCE FROM N.A. (ISOFORM PSMA-1).	R P
	[4]	RN
	J. Neurochem. 69:2270-2277(1997).	<u>г</u> :
	"MOLECULAR CLONING OF A PEPTICASE AGAINST N-ACETYLASPARTYLGLUTAMATE from a rat hippocampal cDNA library ":	7 A
	•	RA
	Bzdega T., Turi T., Wroblewska B., She D., Chung H.S., Kim H.,	RA.
	TISSUE=Prostate; MEDITINE=98041505: DiibMod=9375657:	R R
	SEQUENCE FROM N.A. (ISOFORMS PSMA-1 AND PSMA-2).	RP
•		RN
_	Cancer Res. 55:1441-1443/1995)	RI.
	"Alternatively spliced variants of prostate-specific membrane antigen	R K
-	Su S.L., Huang IP., Fair W.R., Powell C.T., Heston W.D.W.;	RA
	MEDLINE=95188188; PubMed=7882349;	RX
		RC.
	SEQUENCE FROM N.A. (ISOFORM PSMA').	RP K
	Cancer Res. 53:227-230(1993).	RL
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	Eukarvota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	88
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Speno H.S., Luthi-Carter R., Macias W.L. Joshi A.R.T., Coyle J.T., "Site-directed mutagenesis of predicted glutamate carboxypeptidase II."; Mol. Pharmacol. 55:179-185(1999).
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Biochim. Biophys. Acta 1339:247-252(1997).
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MEDLINE=97330810; PubMed=9187245;
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systems.";
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Lupold S.E., Criley S.C., Coffey State: specific membrane antigen.";

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MEDLINE=98288196; PubMed=9622670;
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carcinoma cell line.";
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MEDLINE=99025849; PubMed=9809977;
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Smith A.D., Halsted C.H.;
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Devlin A.M., Ling E.-H., Peerson J.M.,
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J. Pharmacol. Exp. Ther. 286:1020-1025(1998).
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"Molecular cloning of alternatively splice
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                                                              active site residues
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                                                                                                                    Valentine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          human and
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FUNCTION: Has both folate hydrolase and N-acetylated-alpha-linked-acidic dipeptidase (NAALADase) activity. Has a preference for trialpha-glutamate peptides. In the intestine, required for the uptake of folate. In the brain, modulates excitatory neurotransmission through the hydrolysis of the neuropeptide, N-aceylaspartylglutamate (NAAG), thereby releasing glutamate. Stable at pH greater than 6.5. Isoforms PSM-4 and PSM-5 would appear to be physiologically irrelevant. Involved in prostate tumor
progression.
FUNCTION: Also exhibits a dipeptidyl-peptidase IV type activity
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In vitto, cleaves Gly-Pro-AMC.
-!- CATALYTIC ACTIVITY: Release of an unsubstituted, C-terminal glutamyl residue, typically from Ac-Asp-Glu or pteroyl-gamma.
-!- COFACTOR: Zinc; Binds two ions per subunit. Required for NAALADase activity

NAAG, quisqualic acid, 2-(phosphonomethyl) penta (PMPA) and EDTA. Activated by cobalt. SUBCELLULAR LOCATION: Type II membrane protein. The PSMA' isoform is cytoplasmic. ENZYME REGULATION: The NAALADase activity S. pentanedioic inhibited by beta-

Plasma membrane

ALTERNATIVE PRODUCTS:

Event=Alternative splicing: Named isoforms=6; Comment=Experimental confirmation may be la isotorms lacking for

Name=PSMA-Name=PSMA-1; IsoId=Q04609-1; Sequence=Displayed

IsoId=Q04609-2; Sequence=VSP_005341

Name=PSMA-4 Name=PSMA-3 IsoId=Q04609-3; Sequence=VSP_005342,

Name=PSMA-5 IsoId=Q04609-5; IsoId=Q04609-4; Sequence=VSP_005337, Sequence=VSP_005339, VSP_005340; VSP_005338

Name=PSMA IsoId=Q04609-6; Sequence=VSP_005336;

TISSUE SPECIFICITY: Highly expressed in prostate epithelium. Also expressed, in the small intestine, brain, kidney, liver, spleen, colon and the capillary endothelium of a variety of tumors. Expressed specifically in jejunum brush border membranes. In the brain, highly expressed in the ventral striatum and brain stem. I the prostate, the PSMA' cytosolic isoform is the most abundant form in normal tissue, the membrane-bound PSMA-1 form in primary prostate tumors. The PSMA-2 isoform also found in normal prostate as well as in brain and liver.

INDUCTION: In the prostate, up-regulated in response to androgen Also

deprivation.

- i DOMAIN: The NAALADase activity is found in the central region, the dipeptidyl peptidase IV type activity in the C-terminal.

- i PTM: The first two amino acids at the N-terminus of isoform PSMA, appear to be cleaved by limited proteolysis.

- i PTM: The N-terminus is blocked.

- i DISEASE: Defects in FOLH1 may be a cause of hyperhomocysteinemia (HHC), a condition associated with increased risk of (HHC), a condition associated with increased risk of the condition associated with the

MISCELLANEOUS: PSMA is used as a diagnostic and prognostic indicator of prostate cancer, and as a possible marker for neurological disorders such as schizophrenia, Alzheimer's of the control of the con disease various

and Huntington's disease.
SIMILARITY: BELONGS TO PEPTIDASE FAMILY M28B.

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EMBL; M99487; AA EMBL; S76978; AA EMBL; AF007544; ; AAA60209.1; -. ; AAB33750.2; -. 44; AAC83972.1; -

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Matches
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                                           Halsted C.
Gardner J.
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077564;
28-FEB-2003
                                                                                                                                                                                                                                             28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Glutamate carboxypeptidase II (EC 3.4.17.21) (Membrane glutamate carboxypeptidase) (mGCP) (N-acetylated-alpha-linked acidic dipeptidase I) (NAIADase I) (Ptercylpoly-gamma-glutamate carboxypeptidase)
(FOLY)poly-gamma-glutamate carboxypeptidase) (FGCP) (Folate hydrolase I) (Prostate-specific membrane antigen homolog).
            CHARACTERIZATION
                                                                                                               Molecular
                                                                                                                                 Halsted C.H., Ling E.-H., Luthi-Carter Gardner J.M., Coyle J.T.;
                                                                                                                                                       TISSUE-Jejunal mucosa; meDLINE-98352082; pubMed-9685395;
                                                                                                                                                                              SEQUENCE FROM N.A.,
                                                                                                                                                                                                             Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                     Sus scrota (Pig)
 MEDLINE-86085936;
                                                                                                                        "Folylpoly-gamma-glutamate
                                                                                                                                                                                                   NCBI_TaxID=9823;
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Coyle J.T.;
. 275:30746-30746(2000)
                                                                                       273:20417-20424(1998)
                                                                                                                                                                                                                                                                                                                                                              STANDARD;
 PubMed=2867095;
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98.0%;
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                                                     Luthi-Carter
                                                                                                            carboxypeptidase
and relation to c
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Pred. No. 2.7e-162;
5; Mismatches 3;
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carboxypeptidase
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Dipeptidase; Se
Signal-anchor;
DOMAIN 1
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J. Biol. Chem. 261:928-933(1986).
-!- FUNCTION: Has both folate hydrol.
                                                                                                                                                                                                                                                                                                                                                InterPro; IPR003137; PA.
Pfam; PF02225; PA; 1.
Pfam; PF04389; Peptidase_M28;
Pfam; PF04253; TFR_dimer; 1.
Hydrolase; Carboxypeptidase; N
                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                  METAL
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                                                                      CARBOHYD
                                                                                              CARBOHYD
                                                                                                                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AF050502; AAC39269.1; MEROPS; M28.010; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        excitatory neurotransmission through the hydrolysis of the neuropeptide, N-aceylaspartylglutamate (NAAG), thereby releasing glutamate. Maximal activity at pH 6.0.
FUNCTION: Also exhibits a dipeptidyl-peptidase IV type activity (By similarity). In vitro, cleaves Gly-Pro-AMC (By similarity). CATALYTIC ACTIVITY: Release of an unsubstituted, C-terminal glutamyl residue, typically from Ac-Asp-Glu or ptercyl-gamma. COPACTOR: Zinc; Binds two ions per subunit. Required for NAALADase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             jejunum brush-border membrane. Weak expression DOMAIN: The NAALADase activity is found in the dipeptidyl peptidase IV type activity in the C-SIMILARITY: BELONGS TO PEPTIDASE FAMILY M28B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (By similarity).
TISSUE SPECIFICITY: High expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        activity by 50%.
activity by 50%.
SUBCELLULAR LOCATION: Type II membrane protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         acidic dipeptidase (NAALADase) activity. Has a preference alpha-glutamate peptides (By similarity). In the intestine required for the uptake of folate. In the brain, modulates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FUNCTION: Has both folate hydrolase and N-acetylated-alpha-linked-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ENZYME REGULATION: The NAAI quisqualic acid, beta-NAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (PMPA).
           Serine
                                                                                                                                                                                                                                                                                                                           Multifunctional enzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATION: The NAALADase activity is inhibited by cid, beta-NAAG and 2-(phosphonomethyl) pentanedioic Ethanol ingestion decreases the folate hydrolase
            т.т.,
                                                                                                                                                                                                                                                                                                               19
                                                                                                                                                                                                                                                                                                                                       protease; Transmembrane;
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                                                                                                                                      NUCLEOPHILE (NAALADASE) (BY SIN CHARGE RELAY SYSTEM (POTENTIAL) ZINC 2 (BY SIMILARITY).

ZINC 1 (BY SIMILARITY).

ZINC 1 (BY SIMILARITY).

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NAALADASE.
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OR (TYPE-II MEMBRANE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 jejunal brush borders.
                                                                                                                                                                                                                                                                            (POTENTIAL)
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central region,
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AA;

M.

CRC64;

Query Match Best Local (

Local

Similarity

91.3%;

Score 2126; Pred. No. 2.

; DB 1; ?.9e-150;

Length 751; Indels

0;

Gaps

Matches

397;

Conservative

21;

Mismatches

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28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 42, Last sequence update)
28-FEB-2003 (Rel. 42, Last annotation update)
15-SEP-2003 (Rel. 42, Last annotation update)
Glutamate carboxypeptidase II (EC 3.4.17.21) (Membrane glutamate carboxypeptidase) (mGCP) (N-acetylated-alpha-linked acidic dipeptidase I) (NALIADase I) (Pteroylpoly-gamma-glutamate carboxypeptidase) (FGCP) (Folate hydrolase (FOLY)-poly-gamma-glutamate carboxypeptidase) (FGCP) (Folate hydrolase (FOLY)-serate-specific membrane antigen homolog).
                                                Luthi-Carter R., Berger U.V., Barczak A.K., "Isolation and expression of a rat brain cDI carboxypeptidase II.";
                                                                                             MEDLINE=98169524; PubMed=9501243; Luthi-Carter R., Berger U.V., Barcza
                                                                                                                                                                                                                                                     "Molecular cloning of a peptidase agai
from a rat hippocampal cDNA library.";
J. Neurochem. 69:2270-2277(1997).
                                                                                                                                                                                                                                                                                                                                                                           STRAIN-Sprague-Dawley: TISSUE-Hippocampus;
MEDLINE-98041505; PubMed-9375657;
Bzdega T., Turi T., Wroblewska B., She D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mammalia; Eutheria;
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rattus norvegicus (Rat).
                                                                                                                                                                                                    SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chordata;
Rodentia;
                              U.S.A.
                                                                                                                                                                                                                                                                                                                       peptidase against N-acetylaspartylglutamate
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Sciurognathi;
                           95:3215-3220(1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         752
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thi; Muridae; Murinae; Rat
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                                                                                    cDNA encoding
                                                                                                                Enna M.,
                                                                                                                Coyle J.T.;
                                                                                 glutamate
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MEDLINE-96149377; pubMed-8570628;
Carter R.E., Feldman A.R., Coyle J.T.;
"Prostate-specific membrane antigen is a hydrolase w
pharmacologic characteristics of a neuropeptidase.";
Proc. Natl. Acad. Sci. U.S.A. 93:749-753(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- FUNCTION: Also exhibits a dipeptidyl-peptidase IV type activity (By similarity). In vitro, cleaves Gly-Pro-AMC (By similarity).
-!- CATALYTIC ACTIVITY: Release of an unsubstituted, C-terminal glutamyl residue, typically from Ac-Asp-Glu or pteroyl-gamma.
-!- COFACTOR: Zinc; Binds two ions per subunit. Required for NAALADO
                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 284-752 TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ALTERNATIVE SPLICING.
Bzdega T., She D., Turi T., Wroblewska B., Neale J.H.;
"Molecular cloning of alternatively spliced variants of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Luthi-Carter R., Berger Submitted (DEC-1997) to
                                                                                                                                 or send
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        <del>-</del>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            against N-acetylaspartylglutamate (NAAG) from human and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 284-752 FROM N.A.
                                                                                                                                                     entities
                                                                                                                                                                                                                                                                                  TISSUE SPECIFICITY: Widely expressed throughout brain regions with highest levels in the hippocampus, dentate gyrus, priform cortex, choroid plexus of venticles, pineal gland, anterior lobe of the pituitary gland and supraoptic nucleus. High levels also found in the cerebral cortex, substantia nigra, pontine nucleus and the granule cell layer of cerebellum. Highly expressed in astrocytes and non-myelinating Schwann cells. Also expressed in kidney, localizing to the proximal brush border of the renal tube. DOMAIN: The NAALADase activity is found in the central region, the dipeptidyl peptidase IV type activity in the C-terminal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FUNCTION: Has both folate hydrolase and N-acetylated-alpha-linked-acidic dipeptidase (NAALADase) activity. Has a preference for trialpha-glutamate peptides (By similarity). In the intestine, required for the uptake of folate. In the brain, modulates excitatory neurotransmission through the hydrolysis of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ENZYME REGULATION: The NAALADase activity is inhibited by beta-
NAAG, quisqualic acid and 2-(phosphonomethyl)glutaric acid (PMG
SUBCELLULAR LOCATION: Type II membrane protein. Plasma membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Name=3; Synonyms=Long form;
IsoId=P70627-3; Sequence=Not described;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Event=Alternative splicing; Named isoforms=3;
Comment=Experimental confirmation may be la
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ALTERNATIVE PRODUCTS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (By similarity)
                                                    AF040256;
AF039707;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ame=2; Synonyms=Short form;
IsoId=P70627-2; Sequence=Not
Note=Probably inactive;
                                                                                            U75973; AAC53423.1; -.
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                                                                                                                                 an
                                                                                                                                 requires a license agreement (S
an email to license@isb-sib.ch).
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                                                      AAB96759.1;
                                                                          AAC40067
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to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence=Displayed
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     described;
                                                                                                                                                       (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Enna M., Coyle
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MEROPS; M28.010;

IPR003137; PA. 2225; PA; 1.

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RESULT 4
FOH1_MOUSE
ID FOH1_MOUSE STANDARD;
AC 035409; Q9DCC2;
DT 28-FEB-2003 (Rel. 41, Created)
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1 1 CYTOPLASMIC (POTENTIAL).
TRANSMEM 20 44 SIGNAL-ANCHOR (TYPE-II MEMBRANI
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                                                                                                                                                                                                                                                                                                                     DRYVILGGHRDSWVFGGIDPQSGAAVVHETVRSFGTLKKEGWRPRRTILFASWDAEEFGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MGGSAPPDSSWRGSLKVSYNVGPGFTGNFSTQKVKMHIHSTNEVTRIYNVIGTLRGAVEP
                                                                                                                                                                                                                                                              MFLERAFIDPLGLPDRPFYRHVIYAPSSHNKYAGESFPGIYDALFDIESKVDPSKAWGDV
                                                                                                                                                                                                                                                                                                                                                                                                     MGGSAPPDSSWKGGLKVPYNVGPGFAGNFSKQKVKLHIHSYNKVTRIYNVIGTLKGAVEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LGSTEWAEDNSRLLQERGVAYINADSSIEGNYTLRVDCTPLMYSLVYNLTKELKSPDEGF
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                                                                                                                                                      KRQISIAAFTVQAAAETLREV
                                                                                                                                                                                             KRQISVAAFTVQAAAETLSEV
                                                                                                                                                                                                                                      MYLERAFIDPLGLPGRPFYRHIIYAPSSHNKYAGESFPGIYDALFDINNKVDTSKAWREV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EGKSLYDSWKEKSPSTEFIGMPRISKLGSGNDFEVFFQRLGIASGRARYTKNWKNNKVSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EGKSLYESWTKKSPSPEFSGMPRISKLGSGNDFEVFFQRLGIASGRARYTKNWETNKFSG
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87.1%;
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NUCLEOPHILE (NAALADASE) (
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CHARGE RELAY SYSTEM (POTE
CHARGE RELAY SYSTEM (POTE
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ZINC 1 (BY SIMILARITY).
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N-LINKED (GL
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Pred. No. 8
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EXTRACELLULAR (POTENTIAL).
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RAGE RELAY SYSTEM (POTENTIAL)
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C 1 (BY SIMILARITY).
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8.4e-146;
hes 28;
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RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Arakawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Sasaki H., Sato K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.,
RTMINITARINA M., Schotsuki S.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA RAYashizaki Y.,
(By similarity).

-! TISSUE SPECIFICITY: Expressed predominantly in the nippurumeration of the brain and in kidney. Lower levels in the ovary, testis and mandibular gland.
-! DOMAIN: The NAALADase activity is found in the central region, the dipeptidyl peptidase IV type activity in the C-terminal.
-! SIMILARITY: BELONGS TO PEPTIDASE FAMILY M28B.
-! CAUTION: There are amino acid differences between the sequence shown in fig.1 (Ref.1) and the sequence deposited in the database (AF026380). The sequence from fig.1 shows only 3 conflicts between Ref.1 and Ref.2. These are at AA positions 141, 240 and 287.
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28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Glutamate carboxypeptidase II (EC 3.4.17.21) (Membrane glutamate carboxypeptidase) (mGCP) (N-acetylated-alpha-linked acidic dipeptidase I) (NALADase I) (Ptercylpoly-gamma-glutamate carboxypeptidase)
(FOLY-gamma-glutamate carboxypeptidase) (FGCP) (Folate hydrolase I) (Prostate-specific membrane antigen homolog).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN-NIH Swiss; TISSUE-Brain;
STRAIN-NIH Swiss; TISSUE-Brain;
MEDLINE-21077522; PubMed-11210180;
MEDLINE-21077522; PubMed-11210180;
MEDLINE-21077522; PubMed-1120180;
Heston W.D.W.;
"Cloning, expression, genomic localization, and enzymatic activities
"Cloning, expression, genomic localization, and enzymatic activities
of the mouse homolog of prostate-specific membrane antigen/NAALADase/
folate hydrolase.";
folate hydrolase.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Functional annotation of a full-length mouse cDNA collection.";
Nature 409:685-690(2001).

-i- FUNCTION: Has both folate hydrolase and N-acetylated-alpha-linked-acidic dipeptidase (NAALADase) activity. Has a preference for trialpha-glutamate peptides (By similarity). In the intestine, required for the uptake of folate. In the brain, modulates excitatory neurotransmission through the hydrolysis of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=C57BL/6J; TISSUE=Kidney; MEDLINE=21085660; PubMed=11217851;
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                                                                                                                                                                                                                                                                                                                                         activity.

activity.

activity.

ENZYME REGULATION: The NAALADase and are inhibited by quisqualic acid.

Type II membrar
                                                                                                                                                                                                                                                                                                                                                                                                                                                  neuropeptide, N-aceylaspartylglutamate (NAAG), thereby releasing lutamate.

FUNCTION: Also exhibits a dipeptidyl-peptidase IV type activ. (By similarity). In vitro, cleaves Gly-Pro-AMC (By similarit) (CATALYTIC ACTIVITY: Release of an unsubstituted, C-terminal glutamyl residue, typically from Ac-Asp-Glu or pteroyl-gamma COFACTOR: Zinc; Binds two ions per subunit. Required for NAAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FROM N.A.
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Sciurognathi; Muridae
                                                                                                                                                                                                                                                                                                                                                 membrane
                                                                                                                                                                                                                                                                                                                                                                                                     folate
                                                                                                                                                                                                                                                                                                                                                 protein.
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                                                                                                                                                                                                                                                                                                                                                                                                   hydrolase activities
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d, C-terminal
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; Murinae; Mus
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METAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Signal-anchor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hydrolase; Carboxypeptidase; Metalloprotease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam;
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                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                         METAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GO:0005887; C:integral to plasma membrane; IDA.
GO:0008464; F:gamma-glutamyl hydrolase activity; IDA.
GO:0004237; F:membrane dipeptidase activity; IDA.
GO:0006760; P:folic acid and derivative metabolism; IDA.
erPro; IPR003137; PA.
m; PF02225; PA; 1.
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                                                                                                                                                                                                                                          MGGSAPPDSSWRGSLKVSYNVGPGFTGNFSTQKVKMHIHSTNEVTRIYNVIGTLRGAVEP
                                      EGKSLYDSWKEKSPSPEFIGMPRISKLGSGNDFEVFFQRLGIASGRARYTKNWKTNKVSS
                                                                                       EGKSLYESWTKKSPSPEFSGMPRISKLGSGNDFEVFFQRLGIASGRARYTKNWEINKFSG
                                                                                                                           LGSTEWAEEHSRLLQERGVAYINADSSIEGNYTLRVDCTPLMYSLVYNLTKELQSPDEGF
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DKIYNISMKHPQEMKTYSLSFDSLFSAVKNFTEIASKFSERLQDFDKSNPILLRWMNDQL
                        YPLYHSVYETYELVVKFYDPTFKYHLTVAQVRRAMVFELANSIVLPFDCQSYAVALKKYA
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ifunctional enzyme.
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Glycoprotein;
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28-FEB-2003 (Rel. 41, Last annotation update)
N-acetylated-alpha-linked acidic dipeptidase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pangalos M.N., Neefs J.-M., Somers M., Verhasselt P., Bekkers M., van der Helm L., Fraiponts E., Ashton D., Gordon R.D.; "Isolation and expression of novel human glutamate carboxypeptidases with N-acetylated alpha-linked acidic dipeptidase and dipeptidyl peptidase IV activity.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restructe by non-profit institutions as long as its content modified and this statement is not removed. Usage by and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAALAD2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              098300;
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                       TISSUE=Lung carcinoma;
MEDLINE=99185063; PubMed=10085079;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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                                                                                                                                 EMBL; AJ012370; CAB39967.1; -.
                                                                                                                                                             entities requires a license agreement (S or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (NAALADase II).
                                                                                                                                                                                                                                                                                                                                                                                                                                Biol. Chem. 274:8470-8483(1999).

FUNCTION: Has N-acetylated alpha-linked-acidic dipeptidase (NAALADase) activity. Also exhibits a dipeptidyl-peptidase activity. In vitro, cleaves Gly-Pro-AMC.

CATALYTIC ACTIVITY: Release of an unsubstituted, C-terminal Chempyl residue, typically from Ac-Asp-Glu or pteroyl-gamm glutamyl residue, typically from Ac-Asp-Glu or pteroyl-gamm glutamyl residue, typically from Ac-Asp-Glu or pteroyl-gamm
                                                                                                                                                                                                                                                                      putamen and superior colliculus.

DOMAIN: The NAALADase activity is found in the dipeptidyl peptidase IV type activity in the SIMILARITY: BELONGS TO PEPTIDASE FAMILY M28B.
                                                                                                                                                                                                                                                                                                                                                                  SUBCELLULAR LOCATION: Type II membrane protein (Potential). TISSUE SPECIFICITY: Highest expression in the testis. Also
                                                                                                                                                                                                                                                                                                                                                                                                                         COFACTOR: Zinc; Binds two ions per
                                                                                                                                                                                                                                                                                                                            in ovary and spleen. Weak expression in prostate, heart
placenta. In brain, expressed in striatum, parietal cort
ventral striatum with lower levels in hippocampus, brain
                                                                                                                                                                                                                                                                                                                                                                                               ENZYME REGULATION:
                                                                                                                                                                                                                                                                                                                                                                                                             activity.
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Required for NAALADase
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28-FEB-2003 (Rel. 41, Last sequence
P 28-FEB-2003 (Rel. 41, Last annotation
N-acetylated-alpha-linked acidic di
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Best Local
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                                                                                                                                    KKHISIAAFTIQAAAGTLKEV
                                                                                                                                               KRQISVAAFTVQAAAETLSEV
                                                                                                                                                                            MFLERAFIDPLGLPDRPFYRHVIYAPSSHNKYAGESFPGIYDALFDIESKVDPSKAWGDV
                                                                                                                                                                                                                     ASIYNLSKKHDQQLTDHGVSFDSLFSAVKNFSEAASDFHKRLIQVDLNNPIAVRMMNDQL
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ZINC 2 (BY SIMILARITY).
ZINC 1 AND 2 (BY SIMILARITY).
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Pred. No. 1.
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RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Battalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schrim L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Gustincich S., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sazaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Wilming L.,
RA Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.,
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                       the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                         Signal-anchor; NON_TER
                                                                                                                                                                                                                                                                                            Pfam; PF04389; Peptidase_M28; Pfam; PF04253; TFR_dimer; 1.
                                                                                                                                                                                                                                                                                                                                  MEROPS; M28.012; -. MGD; MGI:1919810; Naalad2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Embryo;
                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                        Hydrolase; Carboxypeptidase; Metalloprotease; Dipeptidase; Serine protease; Transmembrane; (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     between
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CATALYTIC ACTIVITY: Release of an unsubstituted, C-terminal glutamyl residue, typically from Ac-Asp-Glu or pteroyl-gamma. COFACTOR: Zinc; Binds two ions per subunit. Required for NAALADase activity (By similarity).
SUBCELLULAR LOCATION: Type II membrane protein (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN: The NAALADase activity is found in the central r dipeptidyl peptidase IV type activity in the C-terminal. SIMILARITY: BELONGS TO PEPTIDASE FAMILY M28B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (NAALADase) activity (By similarity). Also exhibits a dipeptidyl-peptidase IV type activity. In vitro, cleaves Gly-Pro-AMC (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          similarity)
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167; Conserv
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257 i
   Conservative
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173
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120
                     39.3%;
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                                                                    NAALADASE.
CHARGE RELAY SYSTEM (POTEN:
CHARGE RELAY SYSTEM (POTEN:
CHARGE RELAY SYSTEM (POTEN:
ZINC 1 (BY SIMILARITY).
N-LINKED (GLCNAC. . . ) (POTEN:
N-LINKED (GLCNAC. . . )
                     Score 916;
Pred. No. 5
                                                                                                                                                                                                                                           enzyme.
   Mismatches
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                                                                                                                                                                                                                                                            Glycoprotein;
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                                    Length 257;
                                                                                                                                               (POTENTIAL).
(POTENTIAL).
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                                                                                                                                                       the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce) or send an email to license@isb-sib.ch).
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28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
N-acetylated-alpha-linked acidic dipeptidase like protein
(EC 3.4.17.21) (NAALADase L) (Ileal dipeptidylpeptidase) (100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=10116;
 Dipeptidase; S
Signal-anchor;
                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Shneider B.L., Thevananther S., Moyer M.S., Walters H.C., Devarajan P., Sun A.Q., Dawson P.A., Ananthanarayanan M.; "Cloning and characterization of a novel peptidase from r:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=Sprague-Dawley; TISSUE-Ile MEDLINE-98049571; PubMed-9388249;
                               Hydrolase; Carboxypeptidase; Metalloprotease;
                                                Pfam;
                                                                                                InterPro;
                                                                                                            MEROPS; M28.011;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ileum."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Biol.
                                                                                                                                                                                                                                                                                                                                                  Cleaves Gly-Pro-AMC.

CAPALITIC ACTIVITY: Release of an unsubstituted, C-terminal glutamy! residue, typically from Ac-Asp-Glu or ptercyl-gamma. COFACTOR: Zinc; Binds two ions per subunit (By similarity). SUBCELLULAR LOCATION: Type II membrane protein. Ileal brush b
                                                                                                                                                                                                                                                                                        intestine.
SIMILARITY: BELONGS TO PEPTIDASE FAMILY M28B.
                                                                                                                                                                                                                                                                                                                      TISSUE SPECIFICITY: Mainly expressed in the distal small
                                                                                                                                                                                                                                                                                                                                                                                                                                  FUNCTION: Has no NAAG hydrolyzing activity (By similarity). Exhibits a dipeptidyl-peptidase IV type activity. In vitro,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     431
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   311
                                              PF02225; PA; 1.
PF04389; Peptidase_M28;
PF04253; TFR_dimer; 1.
                                                                                                                              AF009921; AAB87644.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   66
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VQAAAETLSEV 441
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                                                                                                IPR003137; PA.
                Serine
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   rine protease;
Multifunctional
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Rodentia;
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                Transmembrane;
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enzyme
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                Glycoprotein;
                               Zinc; Aminopeptidase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Euteleostomi;
; Murinae; Rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     rat
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RESULT NLDL_HU

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Q9UQQ1; 043176; 28-FEB-2003 (Rel. 41, Created) 28-FEB-2003 (Rel. 41, Last sequence update) 28-FEB-2003 (Rel. 41, Last annotation update) N-acetylated-alpha-linked acidic dipeptidase like protein (EC 3.4.17.21) (NAALADase L) (Ileal dipeptidylpeptidase) (100

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                  405
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                                                                                                                                                                                                                                                                                              187;
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                                                                                                                                                                                                                                                                                                      Similarity
                                                                                 YAVVLRKYADKIYNISMKHPQE-----MKTYSLSFDSLFSAVKNFTEIASKFSERLQDFD |: |: |: | | :|: | | :|: |
                                                                                                                    ETNKFSG--YPLYHSVYETYELVEKFYDPMFKYHLTVAQVRGGMVFELANSIVLPFDCRD
                                                                                                                                                                                                                                VEPDRYVILGGHRDSWVFGGIDPQSGAAVVHETVRSFGTLKKEG-WRPRRTILFASWDAE
                                                                                                                                                                                                                                                           LNGTSAPD-SWQGALGCEYKLGPGFEPNGNFPAGSEVKVSVYNRLELRNSSNVLGIIQGA
         FDIESKYDPSKAWGDVKRQISVAAFTVQAAAETLSEV
: ::|| :||:||:|| :: || || ||
                                                                      YSETLQSF------LQAAQENLGALLESHNISLGPLVTAVEKFKAAAAALNQHILTLQ
                                                                                                                                             --GSSGLSIYDNWIRYTNRS-SPVYGLVPSMGTLGAGSDYASFIHFLGITSMDLAYT--Y
                                                                                                                                                               DEGFEGKSLYESW----TKKSPSPEFSGMPRISKLGSGNDFEVFFQRLGIASGRARYTKNW
                                                                                                                                                                                                   EFGLLGSTEWAEDNSRLLQERGVAYINADSSIEGNYTLRVDCTPLMYSLVYNLTKELKSP
ARAQEINSGAEAWAEVERQLSIAVMALEGAAATLQPV
                                   KS--NPILLRMMNDQLMFLERAFIDPLGLPDRPFYRHVIYAPSSHNKYAGESFPGIYDAL
                                                                                                           DRSKTSARIYPTYHTAFDTFDYVEKFLDPGFSSHQAVARTAGSVLLRLSDSLFLPLNVSD
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ZINC 2 (POTENTIAL).

ZINC 1 (BY SIMILARITY).

ZINC 1 (BY SIMILARITY).

ZINC 1 (BY SIMILARITY).
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Pred.
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N-LINKED
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SIGNAL-ANCHOR (TYPE-II MEMBRANE
                                                                                                                                                                                                                                                                                                                                           N-LINKED
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAALADASE.
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-LINKED (GLCNAC...) (PI
-LINKED (GLCNAC...) (PI
A59C2EFD23BE36B5 CRC64;
                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                       882.5;
No. 6.
                                                                                                                                                                                                                                                                                                                                                                   ; DB 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (NAALADASE) (BY SIMILARITY).
SYSTEM (POTENTIAL).
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                                                                                                                                                                                                                                                                                              140;
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                   441
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                                                                                                                                                                                                                                                                                                               745;
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                                                                                                                                                                                                                                                                                              Gaps
                                      705
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                                                                                                                                                                                                                                                            361
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brush border membrane protein) (I100)

, 11 ° n.g; ...

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J. Biol. Chem. 272:31006-31015(1997).

- FUNCTION: NAALADase-like activity unknown. Has no NAAG hydroly activity. Exhibits a dipeptidyl-peptidase IV type activity. If vitro, cleaves Gly-Pro-AMC (By similarity).

- CAPALYTIC ACTIVITY: Release of an unsubstituted, C-terminal glutamyl residue, typically from Ac-Asp-Glu or pteroyl-gamma.

- COPACTOR: Zinc; Binds two ions per subunit (By similarity).
                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entropean Bioinformatics Institute. There are no restructe by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entitles requires a license agreement (See http://www.isb-sorsend an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             with N-acetylated alpha-linked acidic dipeptidase and dipeptidyl peptidase IV activity.";
J. Biol. Chem. 274:8470-8483(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pangalos M.N., Neefs J.-M., Somers M., Verhasselt P., Bekkers M., van der Helm L., Fraiponts E., Ashton D., Gordon R.D.; van der Helm L., Fraiponts E., Ashton D., Gordon R.D.; "Isolation and expression of novel human glutamate carboxypeptidases"
InterPro; IPR003137; PA.
Pfam; PF02225; PA; 1.
Pfam; PF04389; Peptidase_M28; 1.
                                                                                                                                                    EMBL; AJ012371; CAB39968.1; EMBL; AF010141; AAB87645.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Shneider B.L., Thevananther S., Moyer M.S., Walters H.C., Rinaldo Devarajan P., Sun A.Q., Dawson P.A., Ananthanarayanan M.; "Cloning and characterization of a novel peptidase from rat and h
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Small intestine;
MEDLINE=99185063; PubMed=10085079;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ileum brush border mem
NAALADL OR NAALADASEL.
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                                                                                                                           MEROPS;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ISOID=U9UQQ1-8; Sequence=VSP_005352, VSP_005353; TISSUE SPECIFICITY: Mainly expressed in the distal small intestine. Also expressed in the spleen and testis. Weak expression in the brain, locating mainly to the brain sto amygdala, thalamus and ventral striatum. Isoforms 2 and found in the small intestine and anyone in the small intestine and anyone.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             found in the small intestine and colon. SIMILARITY: BELONGS TO PEPTIDASE FAMILY M28B.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Name-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Event-Alternative splicing; Named isoforms=8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ALTERNATIVE PRODUCTS:
                                                                                      602640;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IsoId-Q9UQQ1-7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IsoId=Q9UQQ1-2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IsoId=Q9UQQ1-1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IsoId=Q9UQQ1-6;
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                                                                                                                     M28.011;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence-VSP_005350, VSP_005351;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence=VSP_005348,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence=VSP_005346, VSP_005347;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence=VSP_005344;
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DOMAIN

CYTOPLASMIC (POTENTIAL).
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                                                                                                                                                                                                                                                                   Local
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                                                                                                                                                                                                                                                      185;
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                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                    LNGTLAP-ATWQGALGCHYRLGPGFRPDGDFPADSQVNVSVYNRLELRNSSNVLGIIRGA
                                                                                                                                                                                         MGGSAPPDSSWRGSLKVSYNVGPGF--TGNF-STQKVKMHIHSTNEVTRIYNVIGTLRGA 57
                                      EFGLLGSTEWAEDNSRLLQERGVAYINADSSIEGNYTLRVDCTPLMYSLVYNLTKELKSP
                                                                                  VEPDRYVLYGNHRDSWVHGAVDPSSGTAVLLELSRVLGTLLKKGTWRPRRSIVFASWGAE
                                                                                                                        VEPDRYVILGGHRDSWVFGGIDPQSGAAVVHETVRSFGTLKKEG-WRPRRTILFASWDAE 116
  EFGL1GSTEFTEEFFNKLQERTVAY I NVD1SVFANATLRVQGTPPVQSVVFSATKE1RSP
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CHARGE RELAY SYSTEM (POTENTIAL).
CHARGE RELAY SYSTEM (POTENTIAL).
ZINC 2 (BY SIMILARITY).
ZINC 1 AND 2 (BY SIMILARITY).
ZINC 1 (BY SIMILARITY).
ZINC 1 (BY SIMILARITY).
ZINC 1 (BY SIMILARITY).
ZINC 1 (BY SIMILARITY).
                                                                                                                                                                                                                                                 Score 863.5; DB 1;
Pred. No. 1.7e-56;
1; Mismatches 146;
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/FTId=VSP_005351.
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/FTId=VSP_005347.
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PSLGSLGAGSDYAPFVHFLGI ->
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                                                                                                                                                                                                                                                                                                                                                                                                                 (in isoform 8).
/FTId=VSP_005352
                                                                                                                                                                                                                                                                                                                                                                                                                                                            GPLVTAVEKFEAEAAAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (in isoform 7).
/FTId=VSP_005350.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FSSHQAVARTAGSVILRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Missing (in isoform 6).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CAEEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Favello A., Rifkin L., Chiapelli B.;
Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: Release of an unsubstituted, C-terminal glutamyl residue, typically from Ac-Asp-Glu or pteroyl-gamma.
-!- COFACTOR: Zinc; Binds two ions per subunit (By similarity).
-!- SUBCELLULAR LOCATION: Type II membrane protein.
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M28B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Glutamate carboxypeptidase II homolog (EC 3.4.17.21).
                                                                                                                                                                                                                                                                                                               InterPro; IPR03137; PA.
Pfam; PF02225; PA; 1.
Pfam; PF04389; Peptidase_M28; 1.
Pfam; PF04253; TFR_dimer; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                PIR; T30154; T30154.
MEROPS; M28.010; -.
WormPep; R57.1; CE12844.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                        TRANSMEM
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                                                                                                                                                                                                                                                                zinc;
                                                                                                                                                                                                                                                                                        Hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; U88179;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
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                                                                                                                                                                                                                                         hetical protein; Hydrolase; Carboxypeptidase; Metalloprotease; Transmembrane; Glycoprotein; Signal-anchor.
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6 CYTOPI
23 SIGNAL
                 (POTENTIAL).

EXTRACELLULAR (POTENTIAL).

CAPALYTIC (BY SIMILARITY).

NUCLEOPHILE (BY SIMILARITY).

ZINC 2 (BY SIMILARITY).

ZINC 1 (BY SIMILARITY).

ZINC 1 (BY SIMILARITY).

ZINC 2 (BY SIMILARITY).

ZINC 2 (BY SIMILARITY).
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                                               "The Arabidopsis AMP1 gene encodes carboxypeptidase."; Plant Cell 13:2115-2125(2001).
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28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
28-FEB-2003 (Rel. 41, Last annotation update)
28-FEB-2003 (Rel. 41, Last annotation update)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last seque
                                                                                                                       Dennis E.S., Chaudhury A.;
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64 VILGGHRDSWVFGGIDPQSGAAVVHETVRS-FGTLKKEGWRPRRTILFASWDAEEFGLLG
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AINSYDLN---PTKKGLREIINQISIVQYSVICVVNTLRDV 750
                                    AL--FDIESKVDPSKAWGDVKRQISVAAFTVQAAAETLSEV
                                                                        SQNPYDPKHVNAVNERLKSTERCFINPRGVSMHNPSARHVLFSVSDSDSYSSSLMAGVQN
                                                                                                          DKS--NPILLRMMNDQLMFLERAFIDPLGLP-DRPFYRHVTYAPSSHNKYAGESFPGIYD
                                                                                                                                              KTYLPQLKTTISGINVSRSDFEDIRTQYAL----LSKSAQDLLTMSKKFQETIHFTQHSF
                                                                                                                                                                              RKYADKI-----YNISMKHPQEMKT-YSLSFDSLFSAVKNFTEIASKFSERL----QDF
                                                                                                                                                                                                                    DTYPLYHTMYETPFSNIHLLDTDNLSVHKAIGQYWAELAKTFADDVILPMNTTHFASVML
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STRAIN=cv. Landsberg erecta; TISSUE=Siliques; MEDLINE=21434423; PubMed=11549767; Helliwell C.A., Chin-Atkins A.N., Wilson I.W.
a putative glutamate
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II (EC 3.4.17.21).
                                     I.W.,
                                   Chapple
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                                                                                                                                                                                         Tracheophyta
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Columbia;

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PIR; T47631; T47631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                           ycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FUNCTION: May modulate the level of one or more small signaling molecules that have a role in regulating meristem function. CATMALYTIC ACTIVITY: Release of an unsubstituted, C-terminal glutamyl residue, typically from Ac-Asp-Glu or pteroyl-gamma. COFACTOR: Zinc; Binds two lons per subunit (By similarity). SUBCELLULAR LOCATION: Type II membrane protein. TISSUE SPECIFICITY: Expressed in all plant parts. Highest levels in the bolt stem, inflorescence, root and silique. Low level in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CYCD3 expression.
SIMILARITY: BELONGS TO PEPTIDASE FAMILY M28B.
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                                                                                                                                                                                                                                                                                                                                                                                              PF02225; PA; 1.
PF04389; Peptidase_M28;
PF04253; TFR_dimer; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AF357217; AAL03993.1; -. AL138650; CAB77592.1; -.
                                                                                                                                                                                                                                                                                                                                                         Carboxypeptidase; Metalloprotease;
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356
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                                                                                            (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
CATALYTIC.
NUCLEOPHILE (BY SIMILARITY).
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SIGNAL-ANCHOR (TYPE-II
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                        411
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41; Conservative
                                                                                                                                                                                                                                                        GLLGSTEWAEDNSRLLQERGVAYINADSSIEGNYTLRVDCTPLMYSLVYNLTKELKSPDE 178
                                                                                                                                                                                                                                                                                                                                                         MGGSAPPDSSWRGSLKV--SYNVGPGFTGNFSTQKVKMHIHSTNEVTRIYNVIGTLRGAV
                                                                   ILLRMMNDQLMFLERAFIDPLGLPDRPFYRHVIYAPSSHNKYAGESFPGIYDALFDIESK 410
                                                                                                                   YADKIYNISMKHPQEMKTYSLSFDSLFSAVKNFTEIASKFSERLQDF---
                                                                                                                                                               SGYPLYHSVYETYELVEKFYDPMFKYHLTVAQVRGGMVFELANSIVLPFDCRDYAVVLRK
                                                                                                                                                                                                                                                                                       EPDRYVILGGHRDSWVFGGIDPQSGAAVVHETVRSFGTLKKEGWRPRRTILFASWDAEEF
                                                                                                                                                                                                                                                                                                                                         LGGARAP-LEWRNSGRVGPGQRVGPG-----RMVINMTFQGEMKMKKINNVVVTIRGSE
                      VDPSKAWGDVKRQISVAAFTVQAAAETL 438
                                            {\tt AKRRELNDRLMLVERGFLDAEGIKGKEWFKHLVYGPAAEPESKLGFFPGIADAIAMNASE}
                                                                                                                                           ADYPVYHTAFDSYDWMIHNADPLFHRHVAMAGIWGLLGILLADEPLIPFDYISYAEQLQA
                                                                                                                                                                                          --VGLTVEETFKSQN-----NIIQRLSRVDS--DFSGFLHHAGIPSIDMYYG-----
                                                                                                                                                                                                                  GFEGKSLYESWTKKSPSPEFSGMPRISKLGSGNDFEVFFORLGIASGRARYTKNWETNKF
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-GIIEHEIWRVARAIQRASKAL
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31.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZINC 2 (BY SIMILARITY).

ZINC 1 (BY SIMILARITY).

N-LINKED (GLCNAC. . . ) (PO)

E -> K (IN MUTANT STRAIN P)

MISSING (IN REF. 2).

E -> D (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                    Score 592;
Pred. No. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                         -> D (IN REF. 2)
CF9860FA182EB2B5
                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
700
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.3e-36;
                                                                                                                                                                                                                                                                                                                                                                                          162;
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(POTENTIAL)
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ACCOCC PROPERTY OF THE PROPERT
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TFR2_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kawabata H., Yang R., Hirama T., Vuong P.T. Koeffler H.P.;
"Molecular cloning of transferrin receptor transferrin receptor-like family.";
J. Biol. Chem. 274:20826-20832(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                       TISSUE-Erythroleukemia, and Myeloid MEDLINE=99340005; PubMed=10409623;
                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                  FROM
                         N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (Human)
                                                                                                                                                                                                                                                                                                                                                                                                    (ISOFORMS ALPHA AND
                                  (ISOFORM GAMMA).
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Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                             leukemia
                                                                                                                                                                                                                                                                        P.T.,
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S
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Gombart A.F.,

Schattevoy R., Boright A.P., Weber J.,

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Gloeckner G., Scherer S.,
Tsui L.-C., Rosenthal A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              analysis of 650 kb of genomic reveals 17 genes "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Large-scale sequencing of two regions analysis of 650 kb of genomic sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-20264357; PubMed-10802645;
Camaschella C., Roetto A., Cali A.,
Carella M., Majorano N., Totaro A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 1-158 AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Carcinoma, and
                                                                                            VARIANT HFE3 LYS-172.
MEDLINE=21213521; Pub
                                                                                                                                                                                                                                                                                                                                                                                     Blood 97:2555-2560(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                          Roetto A.,
                                                                                                                                                                                                 --
                                                                                                                                                                                                                                                                                                                                                                                                       Noetto A., Totaro A., Piperno A., Piga A.
Cali A., De Gobbi M., Gasparini P., Camas
New muatations inactivating transferrin
 the
                   between
                                                                                                                                                                                                                                                                                                                         SUBCELLULAR LOCATION: Type II membrane protein. SUBCELLULAR LOCATION: Type II membrane protein.
                                                                                                                                                                                                                                                                                                                                                               FUNCTION: Mediates cellular uptake of transfer non-iron dependent manner. May be involved in
                                                                                                                                                                                                                                                                                                                   ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                      hepatocyte function and erythrocyte differentiation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gene TFR2
                                                                                                                                                                                                                                                                                                       Event=Alternative splicing; Named isoforms=3;
                                              hemochromatosis type III affects the putative initiation the beta isoform thus preventing its translation. SIMILARITY: BELONGS TO PEPTIDASE FAMILY M28B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genet.
                                                                           subjects.
MISCELLANEOUS: The variant lys-172 found in hereditary
          European
                  SWISS-PROT entry is copyright. It is produced through a collaboration -
een the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                IsoId=Q9UP52-2; Sequence=VSP_005354;
                                                                                                                                                                                                                                                                                      IsoId=Q9UP52-1; Sequence=Displayed
                                                                                                                                                                                                                                                IsoId=Q9UP52-3; Sequence=VSP_005355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  genes.";
. 8:1060-1073(1998).
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           Swiss Institute of Bioinf
Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      is mutated in
                                                                                                                                                                                                                                                                                                                                                                                                                                    PubMed=11313241;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Embryo;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                370-801 FROM
   institutions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      a new type of haemochromatosis mapping
                                                                                                                                                                                                                                                                                                                                                                                                         Piga A., Longo F., Garozzo (
., Camaschella C.;
sferrin 2 in hemochromatosis
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    as long
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             restrictions
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EMBL; AF053356; AAC78796.1;
EMBL; AK022002; BAB13951.1;
EMBL; AK000421; BAA91153.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GO; GO:0005887; C:integral to plasma membrane; NAS GO; GO:0004998; F:transferrin receptor activity; N. GO; GO:0006826; P:iron ion transport; NAS.
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CARBOHYD
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DISULFID
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                                                                                                                                                                                                                                                                                                                                                    VGSTEWLEGYLSVLHLKAVVYVSLDNAVLGDDKFHAKTSPLLTSLIESVLKQVDSPNH--
                                                                                                                            ADKIYNISMKHPQEMKTYSLSFDSLFSAVKNFTEIASKFSERLQDFDKSNPILLRMMNDQ
                                                                                                                                                                                                                YPLYHSVYETYELVEKFYDPMF-KYHLTVAQVRGGMVFELANSIVLPFDCRDYAVVLRKY
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                                        LMFLERAFIDPLGLP-DRPFYRHVIYAPSSHNKYA-
IMRVEFYFLSQYVSPADSPF-RHIFMGRGDHTLGALLDHLRLLRSNSSGTPGATSSTGFQ 768
                                                                                                                                                                       YPFLHTKEDTYENLHKVLOGRLPAVAQAVAQLAGQLLIRLSHDRLLPLDFGRYGDVVLRH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        801 AA;
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                                                                                      -GDLKARGLTLQWVYSARGDYIRAAEKLRQEIYSSEERDERLTRMYNVR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 462.5;
Pred. No. 1.1
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R -> RIPLSAQV (IN REF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Missing (in isoform /FTId=VSP_005355.
M -> K (IN HFE3).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               D3D3082BA835413A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches 188;
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                                                        -GESFPGIYDALFDI
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В

408

ESKVDPSKAWGDVKRQISVAAFTVQAAAETLS

----FRRQLALLTWTLQGAANALS

791 439

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RA Arakawa T., Hara A., Fukunishi Y., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyo-oka K., Wang K.H., Weltz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 12
TFR2_MOUSE
                Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Strausberg R.L., Feingold E.A., Grouse L.H., Shenmen C.M., Schuler G.D. Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., HOpkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T. Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S. Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=20160931; PubMed=10681454; MEDLINE=20160931; PubMed=10681454; Fleming R.E., Migas M.C., Holden C.C., Waheed A., Britton R.S., Tomatsu S., Bacon B.R., Sly W.S.; "Transferrin receptor 2: Continued expression in mouse liver in face of iron overload and in hereditary hemochromatosis."; Proc. Natl. Acad. Sci. U.S.A. 97:2214-2219(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TFR2_MOUSE STANDARD; PRT; 798 AA. Q9JKX3; Q92016; Q99MQ9; Q9CPT2; Q99MC9: Created) 28-FEB-2003 (Rel. 41, Last sequence update) 15-SEP-2003 (Rel. 42, Last annotation update) Transferrin receptor protein 2 (TfR2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=C57BL/6J; TISSUE=Liver; MEDLINE=21085660; PubMed=11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kawabata H., Germain R.S., Ikezoe T., Tong X., Green E.M., Gombart A.F., Koeffler H.P.; "Regulation of expression of murine transferrin receptor 2."; Blood 98:1949-1954(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
                                                                                                                                                                                                                     MEDLINE=22388257; PubMed=12477932;
                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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MEDLINE-21426540; PubMe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=10090;
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         ., Carninci P., Prange C.,
Abramson R.D., Mullahy S.J.,
Malek J.A., Gunaratne P.H.,
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                                                                             Scheetz T.E.,
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"Comparative analysis of the gene-dense ACHE/TFR2 region on human "Comparative analysis of the gene-dense ACHE/TFR2 region on human chromosome 7q22 with the orthologous region on mouse chromosome 5."; Nucleic Acids Res. 29:1352-1365(2001).

1- FUNCTION: Mediates cellular uptake of transferrin-bound iron in non-iron dependent manner. May be involved in iron metabolism, hepatocyte function and erythrocyte differentiation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S. Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski Y., Schmutz J., Myers R.M., Schein J.E., Jones S.J.M., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences."
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                                                                                                                       expressed in kidney, spleen, brain, lung, heart and mu very low expression in kidney, muscle and heart. DEVELOPMENTAL STAGE: First expressed beween embryo day In the liver, expression increases during development day 13 to adulthood while, in the spleen, levels remained.
                                                                                                                                                                                                                                        Name=3;
IsoId=Q9JKX3-3; Sequence=VSP_005356;
TISSUE SPECIFICITY: Predominantly expressed in liver. Also
throughout development.
INDUCTION: Down-regulated during erythrocyte differentiation.
Expression unchanged by cellular iron status.
SIMILARITY: BELONGS TO PEPTIDASE FAMILY M28B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cytoplasmic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBCELLULAR LOCATION: Type II membrane protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Event-Alternative splicing; Named isoforms-3;
                                                                                                                                                                                                                                                                                                                                                                                IsoId=Q9JKX3-2; Sequence=VSP_005357,
Note=Lacks most of the extracellular
confirmation available;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IsoId=Q9JKX3-1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OF 1-278 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Riemer C., Martindale D.W., Schnupf P., Hardy D.M., Schwartz S., Scherer S.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sci. U.S.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                     VSP_005358;
domain. No
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EMBL; AF222895; AAF37272.1; EMBL; AF207741; AAL05976.1; EMBL; AF207742; AAL05977.1; EMBL; AK004965; BAB23705.1; EMBL; AK004965; BAB23614.1; EMBL; BC013654; AAH13654.1; EMBL; AF312033; AAK28830.1; -This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its the European Bioinformatics Institute. There are no rest use by non-profit institutions as long as its content modified and this statement is not removed. Usage by ar or send entities requires a s requires a license agreement (See http://www.isb-sib.ch/announce/ an email to license@isb-sib.ch). for commercia

Transmembrane; ... Alternative splicing.
1 81

Pfam; PF04389; Peptidase_M28; Pfam; PF04253; TFR_dimer; 1. Transmembrane; Glycoprotein;

Receptor; Signal-anchor; CYTOPLASMIC (POTENTIAL)
SIGNAL-ANCHOR (TYPE-II |

(TYPE-II MEMBRANE PROTEIN)

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MGD; MGI:1354956; Trfr2.

InterPro; IPR003137; PA. Pfam; PF02225; PA; 1.

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RESULT 13
TFR1_RAT
ID TFR1_AC
09937
AC 09937
AC 28-FE
DT 28-FE
DT 28-FE
DT Trans
GN TFRC
OS RATUU
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Best Local
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                                                TFR1_RAT STANDARD; PRT; 622 AA.

Q99376;
Q99376;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Transferrin receptor protein 1 (TfR1) (TR) (Trfr) (Fragment).
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SITE
Eukaryota; Metazoa; Chordata;
Mammalla; Eutheria; Rodentia;
NCBI_TaxID=10116;
[1]
                                    Rattus norvegicus (Rat).
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                                              OR TRFR.
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                                                                                                                                                                                                                                                                                                                                                                                                      GPVAPQE--WKGHLSGSPYRLGPG-----PDLRLVVNNHRVSTPISNIFACIEGFAEP
                                                                                                                                              GAASSRLTAGLGFQESRFRRQLALLTWTLQGAANALS 788
                                                                                                                                                                                                                                                                          YPLYHSVYETYELVEKFYDPMFKYHL----TVAQVRGGMVFELANSIVLPFDCRDYAVV
                                                                                                                                                                                                                                                         YPFLHTKEDTYENLHK----MLRGRLPAVVQAVAQLAGQLLIRLSHDHLLPLDFGRYGDV
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Pred. No. 2.6
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N-LINKED (GLCNAC. ..)
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ENDOCYTOSIS SIGNAL (POTENTIAL).
INTERCHAIN (POTENTIAL).
INTERCHAIN (POTENTIAL).
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                  Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Rattus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REF.
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.6e-26;
                                                                                                                                                                                                                                                                                                                                                                                                                                           185;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2; AF207742).
2; AF207742 AND 5).
2; AF207742).
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Matches 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a coefficient the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
TISSUE=Testis;
MEDLINE=91125359; PubMed=2126342;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   similarity).-i- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M28B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Characterization of rat transferrin receptor cDNA: the regulation of transferrin receptor mRNA in testes and in Sertoli cells in culture."; Mol. Endocrinol. 4:531-542(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Signal-anchor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF04253;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF04389;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR003137; PA. Pfam; PF02225; PA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HSSP; P02786; 1CX8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; M58040;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- PTM: N- and O-glycosylated, phosphorylated and palmitoylated
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Roberts K.P., Griswold M.D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   nervous system (By similarity).
SUBUNIT: Homodimer; disulfide-linked. Binds one transferrin molecule per polypeptide chain (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBCELLULAR LOCATION: Type II membrane protein (By similarity). TISSUE SPECIFICITY: In testis, expressed in Sertoli cells,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            release. The apotransferrin-receptor complex is then recycled to the cell surface with a return to neutral pH and the concomitant loss of affinity of apotransferrin for its receptor. Transferrin receptor is necessary for development of erythrocytes and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            peritubular myoid cells and Sertoli cells.
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                                                                                                                                                                                                                                                                                            57 AVEPDRYVILGGHRDSWVFGGIDPQSGAAVVHETVRSFG-TLKKEGWRPRRTILFASWDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                  GDYGAVGPTEWLEGYLSSLHLKAFTYINLDKVVLGTSNFKVSASPLLYTLMGKIMQDVKH
                                                                                                                                                                                EEFGLLGSTEWAEDNSRLLQERGVAYINADSSIEGNYTLRVDCTPLMYSLVYNLTKELKS
                                                                                                                                                                                                                                                           YEEPDRYIVVGAQRDAWGPGVAKSSVGTGLLLKLAQVFSDMISKDGFRPSRSIIFASWTA
                                                                                                                                                                                                                                                                                                                                                                  MEGNCPPSWNIDSSCK--LELSQN---
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ETNKFSGYPLYHSVYETYELVEKFYDPMFKYHLTVAQVRGGMVFELANSIVLPFDCRDYA
                                                      P---IDGKYLYRNSNWISK--
                                                                                              PDEGFEGKSLY--ESWTKKSPSPEFSGMPRISKLGSGNDFEVFFQRLGIASGRARYTKNW
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TFR_dimer; 1.
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89; Mismatches
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N-LINKED (GLONAC. .) (POTENTIAL).
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N-LINKED (GLCNAC...)
N-LINKED (GLCNAC...)
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CELL ATTACHMENT SITE (POTENTIAL).
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(BY SIMILARITY).
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RESULT 14
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 Pfam; PF04389; Peptidase_M28; 1.
Pfam; PF04253; TFR_dimer; 1.
Transmembrane; Glycoprotein; Receptor; Lipoprotein; Palmitate;
Signal-anchor; Endocytosis; Phosphorylation.
DOMAIN
1 70
TRANSMEM 71 90
SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
                                                                                                                                                                                                                                                                       This SWI
between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Parker J.S.L., Murphy W.J., Wang D., O'Brien S.J., Parrish C.R.;
"Canine and feline parvoviruses can use human or feline transferrir
receptors to bind, enter, and infect cells.";
J. Virol. 75:3896-3902(2001).

1- FUNCTION: Cellular uptake of iron occurs via receptor-mediated
endocytosis of ligand-occupied transferrin receptor into
specialized endosomes. Endosomal acidification leads to iron
release. The apotransferrin receptor complex is then recycled the cell surface with a return to neutral pH and the concomitar
loss of affinity of apotransferrin for its receptor. Transferri
receptor is necessary for development of erythrocytes and the
                                                                                                                                                                                   use by non-profit institutions as long as modified and this statement is not removed. U entitles requires a license agreement (See htt or send an email to license@isb-sib.ch).
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28-FEB-2003
28-FEB-2003
                                                                                                                                         HSSP;
                                                                                                                          InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CANFA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9615;
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                                                                                                                                                                                                                                                   s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                           nervous system (By similarity).
SUBUNIT: Homodimer, disulfide-linked. Binds one molecule per polypeptide chain (By similarity).
SUBCELLULAR LOCATION: Type II membrane protein PTM: N- and O-glycosylated, phosphorylated and
                                                                                                                                                                                                                                                                                                                                                              similarity).
MISCELLANEOUS: Canine and feline
                                                                                                                                                                                                                                                                                                                 SIMILARITY: BELONGS TO PEPTIDASE FAMILY M28B.
                                                                                                                                                                                                                                                                                                                                   feline transferrin receptors and infect cells.
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                                                                                                      PF02225; PA; 1
                                                                                                                                       P02786; 1CX8
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                                                                                                                        IPR003137;
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(Rel. 41, Last sequence update)
(Rel. 41, Last annotation updat)
receptor protein 1 (TfR1) (TR)
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(TR) (TfR) (Trfr).
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                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
RKYADKIYNISMKHPQ---EMKTYSLSFDSLFSAVKNFTEIASKFSERLQDFDKSNPILL
                                                                                                                                                 --TDYPYLGTTMDLYENLNQKIPQLNKMARGAAEVAGQLIMKLTYDLELNLN------y 621
                                                                                                                                                                                                                                                                GLLGSTEWAEDNSRLLQERGVAYINADSSIEGNYTLRVDCTPLMYSLVYNLTKELKSPDE 178
                                                                                                                                                                                                                                                                                                             PDRYVILGGHRDSWVFGGIDPQSGAAVVHETVRSFGTL-KKEGWRPRRTILFASWDAEEF 118
                        PSKAWGD--VKRQISVAAFTVQAAAETLS
                                                                        RMMNDQLMFLERAFIDPLGLP-DRPFYRHVIYAPSSHNKYAGESFPGIYDALFDIESKVD 412
                                                                                                                                                                                                                                                   GAIGATEWLEGYLSSLHLKAFTYINLDKAILGTSNFKVSASPLLYSLLEKTMKDVKHP--
                                                                                                                                                                                                                                                                                                                                                   MEGDCP--SAW-----EIDPSCRLETSSNKNVNLTVNNVLKEIRIFNVFGVIKGFEE
                                                REINDRIMKVEHNFLSPYVSPRDSPF-RHIFWGSGSH-----TLPALVEHL---KLRQK
                                                                                                 EMYNDRILSFVRDMNQFRTDIKEMGLNLQWLYSARGDFFRATSRLTTDYKNAERTNRFVM
                                                                                                                                                                       KFSGYPLYHSVYETYELVEKFYDPMFKYHLTVAQVRGGMVFELANSIVLPFDCRDYAVVL
                                                                                                                                                                                                 -ITGQSLYRDSNWINK-----VEKLSLDNAAFPFLAYSGIPAVSFCFCED----
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27.6%;
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N-LINKED (GLCNAC...) (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. 1.9e-25;
                                                                                                                                                                                                                                                                                                                                                                                                                            Score 445.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PALMITATE (BY SIMILARITY).
PALMITATE (BY SIMILARITY).
PHOSPHORYLATION (BY SIMILARITY).
INTERCHAIN (BY SIMILARITY).
INTERCHAIN (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STOP-TRANSFER SEQUENCE
CELL ATTACHMENT SITE (1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ENDOCYTOSIS SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LIGAND-BINDING (BY
                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches 180;
                        439
  760
                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                         Length
                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                            770;
                                                                                                                                                                                                                                                                                                                                                                                                    57;
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RESULT 15
TFR1_MOUSE
ID TFR1_MOUSE
                                                                                                                                                                                                             Q62351; Q61560;
28-FEB-2003 (Rel
28-FEB-2003 (Rel
28-FEB-2003 (Rel
                                                                                               Transcript (Mouse).

Mus musculus (Mouse).

Mus musculus (Metazoa; Chordata;

Metazoa; Rodentia;

Metazoa; Rodentia;
STRAIN=C57BL/6 X DBA/2; TISSUE=Hematopoietic; Trowbridge I.S., Domingo D.L., Thomas M.L., Cl Submitted (JAN-1991) to the EMBL/GenBank/DDBJ
                                                                                           Eukaryota; Metazoa; Mammalia; Eutheria; NCBI_TaxID=10090;
                                                                                                                                                                                               Transferrin
                                                             SEQUENCE FROM N.A.
                                                                                                                                                                         (Rel. 41, Createo)
(Rel. 41, Last sequence update)
(Rel. 41, Last annotation update)
(Rel. 41, Tast annotation update)
                                                                                                                                                                                                                                                                                           STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             J. Immunol.
[3]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   [2]
SEQUENCE OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     purification based on its physiology, and partial amino
sequence.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 7-19; 158-179; 196-208;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the nervous system.";
Nat. Genet. 21:396-399(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-99206608; PubMed=10192390;
Levy J.E., Jin O., Fujiwara Y., Ku
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequence
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                                            MOD_RES
DISULFID
DISULFID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -i- SUBCELLULAR LOCATION: Type II membrane protein (By similarity).
-i- PTM, N- and O-glycosylated, phosphorylated and palmitoylated (B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FUNCTION
CARBOHYD
CARBOHYD
                                                                                                                                                   SITE
                                                                                                                                                                                                  DOMAIN
SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MGD; MGI:98822; Trfr.
GO; GO:0006879; P:iron ion homeostasis; IMP
InterPro; IPR003137; PA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M28B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Transferrin receptor is necessary for
                                                                                                                       CIPID
                                                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPRU(
Pfam; PF02225;
                                                                                                                                                                                                                                                                                                    TRANSMEM
                                                                                                                                                                                                                                                                                                                                                   Signal-anchor;
                                                                                                                                                                                                                                                                                                                                                                             Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                    Ptam;
                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam;
                                                                                                                                                                                                                                                                                                                              DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FUNCTION: Cellular uptake of iron occurs via receptor mediated endocytosis of ligand-occupied transferrin receptor into specialized endosomes. Endosomal acidification leads to iron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     release. The apotransferrin-receptor complex is then recycled to the cell surface with a return to neutral pH and the concomitant loss of affinity of apotransferrin for its receptor. Transferrin receptor is necessary for development of erythrocytes and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        European Bioinformatics Institute. There are no rest by non-profit institutions as long as its content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       molecule per polypeptide chain (By similarity). SUBCELLULAR LOCATION: Type II membrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           nervous system (By similarity).
SUBUNIT: Homodimer; disulfide-linked. Binds one transferrin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             S29548; S29548.
                                                                                                                                                                                                                                                                                                                                                                                                                              PF04389;
                                                                                                                                                                                                                                                                                                                                                                                                    PF04253;
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                                                                                                                                                                                                                                                                                                                                                                                            Peptidase_M28; 1.
TFR_dimer; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     PA;
                                                                                                                                                                                                                                                                                                                                                        Endocytosis;
                                                                                                                                                                                                                                                                                                                                                                          Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fujiwara Y., Kuo F.,
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CYTOPLASMIC (POTENTIAL).
PHOSPHORYLATION (BY SIMILARITY).
INTERCHAIN (BY SIMILARITY).
INTERCHAIN (BY SIMILARITY).
O-LINKED (GALNAC. .) (BY SIMIL
N-LINKED (GLCNAC. .) (BY SIMIL
                                                                                                                                                                                                                                                                                                                                                                             Receptor; Lipoprotein; Palmitate
                                                                                                                            CELL ATTACHMENT SITE (POTENTIAL).
PALMITATE (BY SIMILARITY).
                                                                                                                                                                             STOP-TRANSFER SEQUENCE
                                                                                                                                                                                                       ENDOCYTOSIS SIGNAL
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LIGAND-BINDING (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                    SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
                                                                                                                                                                                                                                                                                  (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 , Andrews N.C.; development of erythrocytes
  (GALNAC. ..) (BY SIMILARITY). (GLCNAC. ..) (BY SIMILARITY).
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                                                                                                                                                                                                               517
                                                                                                                                                                                                                                      174 KSPDEGFEGKSLY--ESWTKKSPSPEFSGMPRISKLGSGNDFEVFFQRLGIASGRARYTK 231
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729
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                    YEEPDRYYVVGAQRDA-LGAGVAAKSSVGTGLLLKLAQVFSDMISKDGFRPSRSIIFASW
                                                                                                                                                                                                                                                                                                                                                                         MEGSCPARWNIDSSCK--LELSON-----QNVKLIVKNVLKERRILNIFGVIKG
                                                                                                                                                                                                                                                                                                                                                                                                  MGGSAPP----DSSWRGSLKVSYNVGPGFTGNFSTQKVKMHIHSTNEVTRIYNVIGTLRG
                                                                                                                                                                                                                                                                 TAGDEGAVGATEWLEGYLSSLHLKAFTYINLDKVVLGTSNEKVSASPLLYTLMGKIMQDV
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                       IYDALFDIESKVDPSKAWGDVKRQISVAAFTVQAAAETLS
                                                                                                      YNSKLLSF-----MKDLNQFKTDIRDMGLSLQWLYSARGDYFRATSRLTTDFHNAEK
 FNETLE
                                                  TNRFVMREINDRIMKVEYHFLSPYVSPRESPFRHIFWGSGSHTLSALVENLKLRQKNITA
                                                                             SNPILLRMMNDQLMFLERAFIDPLGLPDRPFYRHVIYAPSSHN---
                                                                                                                                 YAVVLRKYADKIYNISMKHPQEMKT----YSLSFDSLFSAVKNFTEIASKFSERLQDFDK
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                                                                                                                                                                                                               KHP---VDGKSLYRDSNWISK--
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                                                                                                                                                                                                                                                                                                                                                                                                                                             18.7%;
26.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MW;
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  ----RNQLALATWTIQGVANALS
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N-LINKED (GLCNAC...
N-LINKED (GLCNAC...
LA -> AL (IN REF. 2).
W -> H (IN REF. 3; AA
W -> I (IN REF. 3; AA
                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 435; DB 1;
Pred. No. 1.2e-24;
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3; AA SEQUENCE).
19 CRC64;
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Search completed: October 4, 2003, 23:22:06
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AL532691 AL532691
CA489356 ACENCOURT
CA976138 ACENCOURT
BG208080 RST27570
BG194269 RST13413
AI050871 cy47b11.x
BG208080 RST22591
BG940823 RST22191
BF940223 RACFOCOURT
CA488428 ACENCOURT
CA488428 ACENCOURT
CA433141 UI-H-COO-AW951407 EST363477
AI766427 wh49h09 x
B1183520 UNL-P-FN-BF438644 RAB89b03
BG2061102 RST25537
BQ027857 UI-H-COO-CB216928 NISC_P410
CB579300 AMGNUNC:N
AA116793 mq24h05 r
AW207840 UI-H-BI2-AI474492 th21d01.x
AI356718 qy47a12.x
N75691 yv29h07.r1
BU74549 ACENCOURT
BM537110 ha78c03.g
N48056 yy99c12.s1
AK012270 Mus muscu
AW000926 wr90e011 x
AI690667 tx15c10.x
AA897668 cy79c02.s1
AK01270 Mus muscu
AW000926 wr90e01.x
AI690667 tx15c10.x
AA897668 cy79c02.s1
AK01270 Mus muscu
AW000926 xy99c12.s1
AK01270 XJ3407.s1
BG28404 CD3404.8
CB31166 CDA50-D11
BG970797 60284048.r
BU265202 603817489

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Result
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Maximum Match 100%
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Perfect score:
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                        Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000)
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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High-efficiency full-length cDNA cloning
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Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus

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Furuno, M., Hanagaki, T., Hara, A., Hayatsu, N., Hiramoto, K.,
Hiraoka, T., Hori, F., Inotani, K., Ishii, Y., Itoh, M., Izawa, M.,
Hiraoka, T., Kato, H., Kawai, J., Kojima, Y., Konno, H., Kouda, M.,
Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K.,
Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y., Okido, T., Owa, C.,
Saito, H., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D.,
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cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Rigenomic Sciences Center and Genome Science Laboratory in RIKEN.
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Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 3003)
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Please visit our web site (http://genome.gsc.riken.go.jp/)
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62.9%;

Score 1253.4; Pred. No. le-1: 0; Mismatches

le-159;

Indels

0;

Gaps

776

300

480

956

1076

1016

420 896

DB 11; 241;

Length 3003;

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XhoI. Host:
                                              AQLAGAKGMILYSDPADYFVPAVKSYPDGWNLPGGGVORGNVLNLINGAGDPLTPGYPA
AQLAGAKGMILYSDPADYFVPAVKSYPDGWNLPGGGVORGNVLNLINGAGDPLTPGYPA
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FAGNFSTQKVKHHIHSYTKVTRIYNVLGTLKAGALEPDRYVILGGHRDAWFGGIDPQS
GAAVVHBIYRSGFGTLKKKGRRPRTTLFASWDAEEFGLLGSTEWAEEHSRLLQERGVA
YINADSSIEGNYTLKVDCTPLMYSLVYNLTKELQSPDEGFEGKSLYDSWKEKSPSPEF
IGMPRISKLGSONDFEVFFQRLGIASGRARYTKNWKTMKVSSYPLYHSVYETTELVVK
FYDPTFKYHLTVAQVRGAWFELANSIVLFBCQSYAVALKKYADTIYNISMKHPGEM
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PPYSAFSPQGTPEGDLVYVNYARTEDFFKLEREMKISCSGKIVIARYGKVFRGNMVKN
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/strain="C57BL/6J"
/db_xref="FANTOM_DB:0610042N21"
/db_xref="NG1:1907173"
/db_xref="taxon:10090"
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/clone_lib="RIKEN full-length enriched mouse cDNA library"
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(SPTR|Q9DCC2, evidence: FASTY, 100%ID, 100%length)
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TCCAAGCAGCCACAACAAGTATGCAGGGGAGTCATTCCCCAGGAATTTATGATGCTCTGTT
                   TGCATTCATTGATCCTTTAGGCTTACCAGGAAGGCCTTTCTACAGGCATATCATCTATGC
                                     AGCATTTATTGATCCATTAGGGTTACCAGACAGACCTTTTTATAGGCATGTCATCTATGC
                                                         AGACAAAAGCAACCCCATATTACTGAGAATTATGAATGACCAGCTGATGTATCTGGAACG
                                                                            TGACAAAAGCAACCCAATATTGTTAAGAATGATGAATGATCAACTCATGTTTCTGGAAAG
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RS Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y., Arakawa, T., Hara, A., Fukunishi, Y., Konno, H., Adachi, J., Fukuda, S., Aizawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamanaka, I., Saito, T., Okazaki, Y., Gojobori, T., Bono, H., Kasukawa, T., Saito, R., Kadota, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T., Fleischmann, W., Gaasterland, T., Gissi, C., King, B., Kochiwa, H., Kuchi, P., Lewis, S., Matsuo, Y., Nikaido, I., Pesole, G., Kuchi, P., Lewis, S., Matsuo, Y., Nikaido, I., Pesole, G., Rughi, P., Tomita, M., Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H., Baldarelli, R., Barsh, G., Blake, J., Boffelli, D., Bojunga, N., Carninci, P., de Bonaldo, M. F., Brownstein, M.J., Bult, C., Fletcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D., Hofmann, M., Hume, D.A., Kamiya, M., Lee, N.H., Lyons, P., Marchionni, L., Mashima, J., Mazzarelli, J., Mombaerts, P., Nordone, P., Ring, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H., Sato, K., Schonbach, C., Seya, T., Shibata, Y., Storch, K.F., Suzuki, H.,
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vative (60.5%; Score 1205.6; 85.3%; Pred. No. 2.6	904		/clone_lib"RIKEN full-length enriched mouse cDNA library" /clone_lib"RIKEN full-length enriched mouse cDNA library" /dev_stage="0 day neonate" /dev_stage="0 day neonate" /note="polytre uvpolytes /compleances exidence encounter" /note="polytre uvpolytes /compleances exidence encounter"	/db_xref="FANTOM_DB:G630038H05" /db_xref="taxon:10090" /clone="g630038H05" /tissue-tupe="cortex"		Please visit our web site for further details. URL:http://genome.gsc.riken.go.jp/ URL:http://fantom.gsc.riken.go.jp/. URL:http://fantom.gsc.riken.go.jp/.	Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse, figures.	0 5	Submitted (16-Apr-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute: 1-7-25 Guchiroccho Teurumi-ku Yokohama	Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.	Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M., Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N., Okazaki,Y., Saito,R., Saito,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H., Sasaki,D., Shipata,K., Shipagawa,A., Shipaki,T., Sano,H., Sasaki,D., Shipata,K., Shipagawa,A., Shipaki,T.	Fukuda, S., Furung, M., Hanagaki, T., Hara, A., Hashizume, W., Harakida, S., Furung, M., Harakida, A., Hashizume, W., Harakida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katuda, T., Katuda, T., Katuda, T., Katuda, T., Katuda, M., Kayai, T., Koldo, S., Konno, H., Kayai, T., Koldo, M., Kayai, M., Kayai, T., Koldo, M., Kayai, T., Koldo, M., Kayai, T., Koldo, M., Kayai, M., Kayai, M., Kayai, M., Kayai, M., Kayai, M., Kay	of 60,770 full-length cDNAs Nature 420, 563-573 (2002) 6 (bases 1 to 2948) Adachi T Aizawa K Akimura T Arakawa T Bono H Carningi D	5 The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team. Analysis of the mouse transcriptome based on functional annotation	Functional annotation of a full-length mouse cDNA collection Nature 409 (6821), 685-690 (2001) 21085660 11217851	Toyo-oka,K., Wang,K.H., Weitz,C., Whittaker,C., Wilming,L., Wynshaw-Boris,A., Yoshida,K., Hasegawa,Y., Kawaji,H., Kohtsuki,S.
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Email: seqref@genoscope.cns.fr Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 5903.r
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CSODN001AF07QP1&cluster=5903.r. Cont
Feng Liang Email : flang@lifetech.com URL :
http://fulllength.invitrogen.com/ InVitroGen Corporation 160
Faraday Avenue Genoscope sequence ID : CSODN001AF07QP1.
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/organism="Homo sapiens"
//organism="Homo sapiens"
//db xref="taxon:9606"
//db xref="taxon:9606"
//clone="CSODNO11K13"
//tissue_type="ADULT BRAIN"
//dev_stage="adult"
//dev_stage="adult"
//clone_lib="Homo sapiens ADULT BRAIN"
//note="Organ: brain; Vector: pcMVSPORT_6; lst strand cDN
//note="Organ: brain; Vector: pcMVSPORT_6; lst strand cDN
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-strand cDNA was digested with Not I and
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                                                                                 TGGTATACAACCTAACAAAAGAGCTGAAAAGCCCTGATGAAGGCTTTGAAGGCAAATCTC
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AL563970 Homo
CSODM001YE22
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Email: segref@genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 5903.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seg=CSODM001BC11NP1&cluster=5903.r. Contact
Feng Liang Email: fliang@lifetech.com URL:
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
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AL563970.2 GI:31287955
EST.
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11,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished
On Feb 15, 2001 this sequence version replaced
Contact: Genoscope
Genoscope Centre National de Sequencage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                         TATACAACCTAACAAAAGAGCTGAAAAGCCCTGATGAAGGCTTTGAAGGCAAATCTCTTT
                                                                                                                                     ATCTATAGAAGGAAACTACACTCTGAGAGTTGATTGTA-CACCACTGATGTACAGCTTGG
                                                                                                                    TACACAACCTAACAAAAGWGCTG - AAAGCCCTGATGAAGGCTTTGAAGGCAAATCTCTTT
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Location/Qualifiers
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/note="organ: liver; Vector: pcMVSPORT_6; lst strand cDNA
/note="organ: liver; Vector: pcMVSPORT_6; lst strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-strand cDNA was digested with Not I and
cloned into the Not I and EcoRV sites of the pcMVSPORT 6
vector. Library was not normalized."
vector. Library was not normalized."
251 c 212 g 333 t 63 others
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/mol_type="mRNA"
/db_xref="taxon:9606"
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/dev_stage="fetal"
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o sapiens FETAL LIVER Homo
3-PRIME, mRNA sequence.
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92.2%;
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AL532691
AL532691.2 GI:3107052
                                 Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates; 1 to 1201
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                                                                                 Homo sapiens
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                                                                                                                               GI:31070523
                           Jessee, J. and Polayes, D.
                                                                                                                                                            mRNA sequence.
                                                                                                                                                                                          1201 bp
                                                       Craniata; Vertebrata; Catarrhini; Hominidae;
                                                                                                                                                                                             mRNA
                                                          Hominidae;
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linear

EST 23-MAY-2003

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Euteleostomi;

Oy 931 AGAGCGTGGCCTGACTTATATATGCTGACTCATCTATAGAAGGAAACTACACTCTGAG Db 941 AGAGCGTGGCGTGGCTTATATTAATGCTGACTCATCTATAGAAGGAAACTACACTCTGAG 941 AGAGCGTGGCGTGGCTTATATTAATGCTMACTCATCTATAGAAGGAAACTACACTCTGAG Oy 991 AGTTGATTGTACACCACTGATGTACAGCTTGGTATACAAACAA	ation about this cluster, see genoscope.cns.fr/ genoscope.cns.fr/ genoscope.cns.fr/ length.invitrogen.com/InVitroGen.Corporation 1600 nue Genoscope sequence ID : CSODNOO1AF07NP1. 1201 rganism="Homo sapiens" ol.type="mrNA" b_xref="taxon:9606" b_xref="taxon:9606" b_xref="taxon:9606" b_xref="taxon:9606" clone="CSODNOO1XF13" lone="CSODNOO1XF13" lone="CSODNOO1XF13" lone="CSODNOO1XF13" lone="Ibb="Homo sapiens ADULT BRAIN" ev_stage="adult" lone_lib="Homo sapiens ADULT BRAIN" lone_lib="Homo sapiens ADULT BRAIN" ev_stage="adult" lone_lib="homo sapiens ADULT BRAIN" lone_lib="homo sapiens" lone_lib="homo sapie	JOURNAL Unpublished On Feb 13, 2001 this sequence version replaced gi:12796184. COMMENT On Feb 13, 2001 this sequence version replaced gi:12796184. Contact: Genoscope Contact: Genoscope Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - France Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 5003.r For
RESULT 6 CA489536 LCCUS LCCUS AGENCOURT_10810626 MAPCL Homo sapiens cDNA clone IMAGE:6722010 5', ACCESSION ACCESSION CA489536.1 GI:24952327 REYWORDS Homo sapiens CORANISM EUKAYYORD, Homo sapiens EUKAYYORD, Homo sapiens CORANISM Homo sapiens EUKAYYORD, Homo sapiens EUKAYYORD, Homo sapiens CORANISM Homo sapiens EUKAYYORD, Homo sapiens EUKAYYORD, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Homo sapiens NATIONALIDATE PRIMATES; Catarrhini; Hominidae; Homo. 1170 REFERENCE 1 (bases 1 to 889) 1 (ba	Db 461 Qy 1470 Db 401 Db 401 Db 341 Qy 1530 Db 341 Qy 1590 Db 298 Qy 1650 Db 298 Qy 1710 Db 254 Qy 1770 Db 1134 B Qy 1889 Db 74 1 Qy 1947 Db 159	Db 581 AAAAGTTTTATGATCCAATGTTTAAATATCACCTCACTGTGGCCCAGGTTCGAGGAGGA 522 Qy 1350 TGGTGTTTGAGCCAAGTCCATAGTGCTCCCTTTTGATTGTCGAGAAGTATGCTGTAG 1409

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                                                         ACAGTTTATCATTTGATTCACTTTTTTCTGCAGTAAAAAATTTTACAGAAATTGCTTCCA 1535
                                                                                                          GAAAGTATGCTGACAAAATCTACAATATTTCTATGAAACATCCACAGGAAATGAAGACAT 1475
AGTTCAGCGAGAGACTCCAGGACTTTGACAAAAGCAACCCAATATTGTTAAGAATGATGA 1595
                                               ACAGTGTATCATTTGATTCACTTTTTTCTGCAGTAAAGAATTTTTACAGAAATTGCTTCCA
                                                                                               GAAAGTATGCTGACAAAATCTACAGTATTTCTATGAAACATCCACAGGAAATGAAGACAT
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Manuscript submitted."
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/clone="IMAGE:6722010"
/cell_line="ZR-75-1, MC
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/mol_type="mRNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tissue Procurement: Dr. James R. Lupski cDNA Library Preparation: Life Technologies, Inc. cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AGENCOURT_8955013 Lupski_sciatic_nerve Homo sapiens cDNA clone IMAGE:6202554 5', mRNA sequence.
CA976138
AAACTACACTCTGAGAGTTGATTGTACACCACTGATGTACAGCTTGGTATACAACCTAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 (bases 1 to 885)
NIH-MCC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: cgapbs-r@mail.nih.gov
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                                                                                                                                                                                      /Clone_lib="Lupski_sciatic_nerve"
/Clone_lib="Lupski_sciatic_nerve"
/note="Vector: pCMV-SPORT6 (Life Technologies); Site_1:
NotI; Site_2: Sall; cDNA made by oligo-dT priming.
Directionally cloned using the following adaptors:
5'-TCGACCACGCGTCCG-3' and
5'-GACTACTTCTRGATCGCGACCGCCCT(15)-3'. Size selected >
1 kb for average insert length 1.87 kb. This is a primary
Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor College of Medicine) and is available through Life
College of Medicine) and is available through Life
                                                                                                                                                                   Technologies."
                                                                                                                                                                                                                                                                                                                                                                              /tissue_type="sciatic nerve"
/dev_stage="adult, 70 yr"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens
/mol_type="mRNA"
/db_xref="taxon:9606"
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Harrington, J.J., Sherf, B., Rundlett, S., Jackson, P.D., Perry, R., Cain, S., Leventhal, C., Thornton, M., Ramachandran, R., Whittington, J., Leventhal, C., McElligott, K., Boozer, S., Mays, R., Smith, Lerner, L., Costa
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Athersys, Inc.
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/note="See 'Creation of Genome-wide Protein Expression',
Libraries using Random Activation of Gene Expression',
Nature Biotechnology, in press. Note that even though the
cell type indicated is HT1080, since a random activation
method was used, these sequence tags are not necessarily
expressed in HT1080 under normal circumstances."
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                                              ACTCTACCAATGAAGTGACGAGAATTTACAATGTGATAGGTACTCTCAGAGGAGCAGTGG
                                                                                                                            ACAATGTTGGACCTGGCTTTACTGGAAACTTTTCTACACAAAAAGTCAAGATGCACATCC
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                     ACTCTACCAATGAAGTGACAAGAATTTACAATGTGATAGGTACTCTCAGAGGAGCAGTGG
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RST13413 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.
BG194269 GI:13715956
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/cell_line="HT1080"
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CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome
Clone distribution: NCI-CGAP clone distribution
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 864 Std Error: 0.00
                                                                                                                                                                                                              Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
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NCI_WINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/BTGAP), Tumor Gene Index
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                                                                                                                                                                                                Tissue Procurement: David
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<u>similar to qb</u>:M99487 PROSTATE-SPECIFIC MEMBRANE ANTIGEN (HUMAN );CONTAINS Alu repetitive element; mRNA common descriptions of the common description description of the common description of the common description of the common description descript
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                                                                                                                                                  cDNA Library Preparation: M. Bento Soares,
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              AGAGACTCTGTATTGAATTTGTGTGGTATGTCACTC - - AAAGAATAATAATGGGTATATT
                                                                   AGCCTTCACAGTGCAGGCAGCTGCAGAGACTTTGAGTGAAGTAGCCTAAGAGGATTCTTT 1866
                                                                                                TGAAAGCAAAGTGGACCCTTCCAAGGCCTGGGGAGAAGTGAAGAGACAGATTTATGTTGC
                                                                                                                                                       CAGCCACAACAAGTATGCAGGGGAGTCATTCCCCAGGAATTTATGATGCTCTGTTTGATAT
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/clone="IMAGE:1668957"
/tissue_type="glioblastoma (pooled)"
/lab_host="DH10B"
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Creation of genome-wide protein expression libraries using random activation of gene expression
activation of gene expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: scain@athersys.com
High quality sequence stop: !
Location/Qualifiers
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RST22191 Athersys RAGE Library Homo
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Fax: 216 361 9596
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                                                                                                                                                                                                                                                                                                                                                                                                  GATAATTCAAGACTCCTTCAAGAGCGTGGC--GTGGCTTATATTAATGCTGACTCATCTA 968
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                                                                                                                                                                                                                                                                                                                                                                      GAGAAACTAAGACTCCTTCTTTAGCGTGGCAGTCGGCTTATATTAATGCTGACTCATCTA
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/Clone_See /Creation of Genome-wide Protein Expression
/note="See /Creation of Genome-wide Protein Expression/
/Interaction of Gene Expression/
Nature Biotechnology, in press. Note that even though the
cell type indicated is H71080, since a random activation
method was used, these sequence tags not necessarily
expressed in H71080 under normal circumstances."
a 151 c 159 g 230 t 1 others
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/db_xref="taxon:9606"
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Pred. No. 2.
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               info@image.llnl.gov
Seq primer: -40UP from Gibco
                             cDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL, send email to:
                                                                                                             Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: David N. Loui
                                                                                   Bonaldo,
                                                                                                                                                           1 (bases 1 to 720)

NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/BTGAP), Tumor Gene Index
                                                                                                                                                                                                                                                                                                BF940223 720 bp mRNA linear EST 22-JAN-2001 nac70c04.x1 NCI_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:4439495 37 similar to SW:PSM_HUMAN Q04609 PROSTATE-SPECIFIC MEMBRANE ANTIGEN
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                                                                                                                                                    Unpublished
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                         cDNA Library Preparation: M. Bento
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                                                                                   Ph.D.
                                                                                                           N. Louis, M.D., Myrna R.
                                                                                        Soares,
                                                                                       Ph.D.,
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                                                  ATTTCTGTTGCAGCCTTCACAGTGCAGGCAGCTGCAGAGACTTTGAGTGAAGTAGCCTAA 1855
                                                                                                                                                                                                               GAAAGAGCATTTATTGATCCATTAGGGTTACCAGACAGGCCTTTTTATAGGCATGTCATC
                                                                                                        CTGTTTGATATTGAAAGCAAAGTGGACCCTTCCAAGGCCTGGGGAGAAGTGAAGAGACAG
                                                                                                                                                           TATGCTCCAAGCAGCCACAACAAGTATGCAGGGGAGTCATTCCCAGGAATTTATGATGCT 1735
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/db_xref="taxon:9606"
/clone="IMAGE:3439495"
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RESULT 13
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ty64912.xl NCI_CGAP_Kidl1 Homo s
similar to gb:M99487 PROSTATE-SP
mRNA securer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Verte
Mammalia; Eutheria; Primates; Catarrhini; Hon
1 (bases 1 to 690)
NCI_CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
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AI672408
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     National Cancer Institute, Cancer Tumor Gene Index
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                                                                                                        CTGTAGTTTTAAGAAAGTATGCTGACAAAATCTACAATATTTCTATGAAAACATCCACAGG
                                                   AAATGAAGACATACAGTTTATCATTTGATTCACTTTTTTCTGCAGTAAAAAATTTTACAG
                                                                                                                                  GAGGGATGGTGTNTGAGCTAGCCATTCCCATAGTGCTCCCTTTTGATTGTCGAGATTATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2283910"
/lab_host="DH10B"
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152 c 110
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                                                                                                                                                                                                                                       Score 625.4; DB pred. No. 5.9e-7 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Robert Strausberg, Ph.D.
Email: cgapbs r@mail.nih.gov
Tissue Procurement: Kristi A. Egland, Ira Pastan
CDNA Library Preparation: Invitrogen Corp
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Biosolence Corporation
Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 (bases 1 to 916)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
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                                                                                                                                                                                                                                                                                                                                                                                                  http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                         found through the I.M.A.G.E. Consortium/LLNL at:
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/clone_lib="MAPCL"
/note="Yector: pCMV-SPORT6; Site_1: EcoRV; Site_2: Not I;
/note="Yector: pCMV-SPORT6; Site_1: EcoRV; Site_2: Not I;
Subtracted with brain, liver, lung, kidney and muscle.
Directionally cloned. Priming method: oligo-dT. Average
insert size: 1800 bp. Library amplification: 26,000 fold
                                                                                                                                                                            /cell
                                                                                                                                                                                                 /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6720185"
                                                                                                                               /lab_host="EMDH10B"
                                                                                                                                                      LNCaP"
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UI-H-COO-ark-a-12-0-UI.Sl NCI_CGAP_Sub9 Homo sapiens
UI-H-COO-ark-a-12-0-UI 3', mRNA sequence.
       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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                                                                                                                                                                                                                                                                                                                      AATTGCTTTCCAGNTCAGTGAGAGAACTCAGGGACTTTGACAAAAGCAACCCCAATAGTAT
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                                                                                                                                                                                                                                                                                                                                    AATTGCTTCCAAGTTCAGCGAGAG-ACTCCAGGACTTTGACAAAAGGAACCCAATATTGT 1583
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(bases 1 to 606)
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                                                                                 GI:24797561
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TITLE
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                     1628 ATTGATCCATTAGGGTTACCAGACAGACCTTTTTATAGGCATGTCATCTATGCTCCAAGC
                                                                                                                                                                                                                                        1508
                                                                                                                                                                                                                                                                                                                                                                  1448 ATGAAACATCCACAGGAAATGAAGACATACAGTTTATCATTTGATTCACTTTTTTCTGCA 1507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Jose Mercuende
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
cDNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be obtained
from Dr. M. Bento Soares, bento-soares@willowa.edu
The following repetitive elements were found in this cDNA
sequence: 1-73, >AT_rich#Low_complexity (matched compliment)
com reference with repearance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                     AGCAACCCAATATTGTTAAGAATGATGAATGATCAACTCATGTTTCTGGAAAGAGCATTT 1627
                                                                                                                                                                                                                          GTAAAAAATTTTACAGAAATTGCTTCCAAGTTCAGCGAGAGACTCCAGGACTTTGACAAA 1567
                                                                                                                                                                                                                                                                            ATGAAACATCCACAGGAAATGAAGACATACAGTGTATCATTTGATTCACTTTTTTCTGCA
  ATTGATCCATTAGGGTTACCAGACAGGCCTTTTTATAGGCATGTCATNTATGCTCCAAGC
                                                                                                                                                                                 POLYA=Yes.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished
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National Cancer Institute, Cancer Genome Anat
                                                                                        AGCAACCCAATAGTATTAAGAATGATGAATGATCAACTCATGTTTCTGGAAAGAGCATTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TAG_TISSUE=Prostate Carcinoma
TAG_SEQ=ATGG"
127 c 90 g 209 t
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/clone_lib="NCI_CGAP_Sub9"
/clone_lib="NCI_CGAP_Sub9"
/note="Vector: p773-Pac (Pharmacia) with a modified
/note="Vector: p773-Pac (Pharmacia) with a modified
polylinker; Site_1: EcoR I; Site_2: Not I; tissues:
Cholonic mucosa with Crohns disease, Cholonic mucosa with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TAG_LIB=UI-H-COO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           information, contact: Bento Soares,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone="UI-H-COO-ark-a-12-0-UI"
/tissue_type="mixed"
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Pred. No. 3.7e-67;
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SUMMARIES

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ALIGNMENTS

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AUTHORS TITLE	REFERENCE	SOURCE ORGANISM	KEYWORDS	VERSION	ACCESSION		DEFINITION	LOCUS	AF261715	RESULT 1
O'Keefe,D.S., Bacich,p.J. and Heston,W.D.W. Cloning and Characterization of a novel glutamate-preferring	<pre>Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to.1992)</pre>	Homo sapiens (human) Homo sapiens		AF261715.1 GI:11078563	AF261715	(PSMAL/GCP III) mRNA, complete cds.	Homo sapiens prostate-specific membrane antigen-like protein	AF261715 1992 bp mRNA linear PRI 02-NOV-2000		

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Unpublished
2 (bases 1 to 1992)
0'Keefe,D.S., Bacich,D.J. and Heston,W.D.W.
Expression Profile of Prostate-Specific Membrane Versus a Prostate-Specific Membrane Antigen-Like
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Submitted (27-APR-2000)
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GGTTAAAAATGCCCAGCTGGCAGGGGCCAAAGGAGTCATTCTCTACTCAGACCCTGCTGA
                                                                                   TAATGACAAAAGGTTGAAGATAAAGTTCTAGTACTCATTTAAGTGTAATATTGAAAATTG
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TRIYNVIGTLRCAVEDDRYVILGGHRDSWVEGGIDPGSGAAVVHETVRSFGTLKEGW
RPRRTILFASWDAEEFGLLGSTEMAEDNSRLLGERGVAYIADSSIEGNYTLKVEGW
RPRRTILFASWDAEEFGLLGSTEMAEDNSRLJCERGVAYIADSSIEGNYTLRVDCTP
LMYSLVVNLTKELKSDDGGFEGKSLYESNTKKSPSPEFSGMPRLSKLGSGNDFRVFFQ
RLGIASGRARYTKNWETNKFSGYPLYHSVYETYELVEKFYDPMFKYHLTVAQVRGGMV
FELANSIVLPFDCRDYANVLRKYADKIINISMKHPGEMXTYSLSFDSLLSAVKNFTEI
ASKFSBRLQDPDKSNPILLRMMNDQLMFLERAFIDPLGLDRPFYRHVIYAPSSHNKY
AGESFPGTYDALFDIESKVDPSKAWGDVKRQISVAAFTVQAAAETLSEVA"
352 c 451 g 551 t
                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="PSMAL/GCP III"
/function="N-acetylated-alpha-linked-acidic dipeptidase"
/function="Glutamate carboxypeptidase III; similar to Homo
/note="glutamate carboxypeptidase III; similar to Homo
sapiens PSMA; folate hydrolase-like; member of the M28
peptidase family; formed by duplication of the PSMA gene
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                   /product="prostate-specific
/protein_id="AAG29102.1"
/db_xref="GI:11078564"
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/chromosome="11"
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/mol_type="mRNA"
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Query Match 85.5%; Score 1702.6; DB 6; Length 2653; Best Local Similarity 98.5%; Pred. No. 0; Matches 1729; Conservative 0; Mismatches 24; Indels 2; Gaps 1; Matches 1729; Conservative 0; Mismatches 24; Indels 2; Gaps 1; Qy 240 AGGTTAAAAATGCCCAGCTGGCAGGGGCCAAAGGAGTCATTCTCTACTCAGACCCTGCTG 299	782 a	JOURNAL Patent: WO 0194629-A 8007 13-DEC-2001; FEATURES Location/Qualifiers SOURCE 1 2653		Eukaryota; Metazoa; Chordata; Craniata; Vertebre Mammalia; Eutheria; Primates; Catarrhini; Homini 1	Z	AX337498 AX337498 AX337498 AX337498 ACCESSION AX337498 ACCESSION AX337498	1981 /	Qy 1981 AAAAAAAAAAA 1992 	OY 1921 TATTGATAAATTTTAAAATTGGTATATTTGAAATAAAGTTGAATATTAT	Qy 1861 TTCTTTAGAGACTCTGTATTGAATTTGTGTGGTATGTCACTCAAAGAATAATAATGAGTA 1920	Db 1801 TGTTGCAGCCTTCACAGTGCAGCTGCAGAGACTTTGAGTGAAGTAGCCTAAGAGA 1860	1741 TGATATTGAAAGCAAAGTGGACCCTTCCAAGGCCTGGGGAGATGTGAAGAGACAGATTTC	Db 1681 TCCAAGCAGCACAACAAGTATGCAGGGGAGTCATTCCCAGGAATTTATGATGCTCTGTT 1740 QY 1741 TGATATTGAAAGCAAAGTGGACCCTTCCAAGGCCTGGGGAGATGTGAAGAGACAGATTTC 1800	1681	Db 1621 AGCATTTATTGATCCATTAGGGTTACCAGACAGACCTTTTTATAGGCATGTCATCTATGC 1680	1561 TGACAAAAGCCAATATTGTTAAGAATGATGAATGATCAACTCATGTTTCTTGGAAAG	Qy 1561 TGACAAAAGCAACCCAATATTGTTAAGAATGATGATGATCAACTCATGTTTCTGGAAAG 1620	QY 1501 TTCTGCAGTAAAAAATTTTACAGAAATTGCTTCCAAGTTCAGCGAGAGACTCCAGGACTT 1560	1441	Qy 1441 TATTTCTATGAAACATCCACAGGAAATGAAGACATACAGTTTATCATTTGATTCACTTTT 1500
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GNFSTQKVKMHIHSTNEVTRIYNVIGTIRGAVEPDRYVILGGHRDSWFFGGIDPQSGA
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Devlin,A.M., Ling,E.H., Peerson,J.M., Fernando,S., C
                                                                                                                                                                                                                                                                                                                                                                                                                      Smith, A.D. and Halsted, C.H.
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/moi_type="maNA"
/db_xref="taxon:9606"
/tissue_type="small intes
1. .2518
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/codon_start=1
/codon_start=1
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/protein_id="AAD51121.1"
/db_xxef="GI:5762482"
/translation="MWNLLHETDSAVATARRPRWLCAGALVLAGGFFLLGFLFGWFIK
                                                                                                    /gene="FGCP"
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Ling, E.-H.
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                        ACTCATCTATAGAAGGAAACTACACTCTGAGAGTTGATTGTACACCACTGATGTACAGCT
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FGLDSVELAHYDVLLSYPNKTHENYISIINEDGNEIFMISLFEPPPPGYENVSDIVP
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GNFSTQKVKMHIHSTNEVTRIYNVIGTLRGAVEPDRYVILGGHRDSWVFGGIDPGSGA
AVVHEIVRSFGTLKKEGWRPRRFILFASWDAEEFGLLGSTEWAEENSRLLQERGVAXI
NADSSIEGNYTLRVDCTPLMYSLVHNLTKELKSPDEGFEGKSLYESWTKKSPSPEFSG
MPRISKLGSGNDFEVFFQRLGIASGRARYTKNWFTNKFSCYPLYHSYVETYELVEKTY
DPMFKYHLTVAGVRGGMYFELANSIVLFDCRDYAVVLKKYADKIYSISMKHPQEMKT
YSVSFDSLFSAVKNFTELASKFSERLQDFDKSNPIVLRMNNDQLMFLERAFIDPLGLD
PRFYTHYLYAPSSHNKYAGESFPGIYDALFDIESKVDPSKAWGEVKRQIYVAAFTVQ
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Secreted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota;
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                                                                                            TTCTGGGAGGTCACCGGGACTCATGGGTGTTTGGTGGTATTGACCCTCAGAGTGGAGCAG
                                                                                                                          CACCACCAGATAGCAGCTGGAGAGGAAGTCTCAAAGTGTCCTACAATGTTGGACCTGGCT
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CACCACCAGATAGCAGCTGGAGAGGAAGTCTCAAAGTGCCCTACAATGTTGGACCTGGCT
                               GAAGAACAATTTTGTTTGCAAGCTGGGATGCAGAAGAATTTGGTCTTCTTGGTTCTACTG
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Eutheria;
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
509 c 623 g 68
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98.6%;
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SSNEARINITPKHNMKAFLDELKAENIKKFLYRFTGIPHLAGTEQNFQLAKOIQSQWKE
FGLDSYELAHYDVLLSYPNKTHENYISIINEDGMEIFNTSLFEPPPPGYENVSDIYVP
FSAFSPQGMPEGDLYYVNYARTEDFFKLERDMKINCSGKIYLARYGKVFRGNKVKNAQ
LAGAKOYILYSDPADYFAPGYKSYPDGWNLPGGGVQRGHLINLNCAGDPLTPGYPANE
YAYRRGIAEANGLESIPVHPIGYYDAQKLEKWGGSAPPDSSWRGSLKVPYNVGPGFT
GNESTQKVKMHIHSTNEVTRIYNVIGTLRGAVEPDRYVILGGHRDSWVFGGIDPQSGA
AVVHEIVRSFGTLKKEGWRPRRTILFASWDAEEFGLLGSTEWAEENSRLLQERGVAXI
NADSSLEEGNYTLRVDCTPLMYSLUVHNITRELKSPDEGFBCKSLLESWTKKSPEPEFSG
MPRISKLGSGNDFEVFFQRLGIASGRARYTKNWETNKFSGYPLYHSVYETYELVEKFY
DPMFKYHLTVAQVRGGWFELANSIVLPHDCTDYAVLTKXADKITSISMKHPQEMKT
TSVSFDSLESAVKNTFELASKFSERLQDPDKSWPIVLRWMNDQLMFLERAFIDDLGLP
DRPFYRHVILAPSSHNKYAGESFPGIYDALFDIESKVDPSKAWGEVKROIYVAAFTVQ
DRPFYRHVILAPSSHNKYAGESFPGIYDALFDIESKVDPSKAWGEVKROIYVAAFTVQ
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/protein_id="CAD42451.1"
/db_xref="GI:21900510"
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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Series:
                                                       Web site: http://www.nisc.nih.gov/
Contact: nisc_mgc@nhgri.nih.gov
Shevchenko,Y., Wetherby,K.D., Beckstrom-Sternberg,S.M.,
Benjamin,B., Blakesley,R.W., Bouffard,G.G., Brinkley,C., Brooks,S.,
Benjamin,B., Guan,X., Gupta,J., Ho,S.-L., Karlins,E., Legaspi,R.,
Lim,M., Maduro,Q.L., Mastello,C., Mastrian,S.D., McCloskey,J.C.,
McDowell,J., Pearson,R., Snyder,B., Stantripop,S., Thomas,P.J.,
Tiongson,E.E., Touchman,J.W., Tsurgeon,C., Vogt,J.L., Walker,M.A.,
Zhang,L.-H. and Green,E.D.
                                                                                                                                                                          cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: National Institutes of Health Intramur Sequencing Center (NISC), Gaithersburg, Maryland; Web site: http://www.nisc.nih.gov/
                                                                                                                                                                                                                                                             NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-remail.nih.gov
Tissue_Procurement: Life Technologies, Inc.
                                                                                                                                                                                                                                                                                                                                Direct Submission
Submitted (06-MAR-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                             Strausberg, R.
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gh the I.M.A.G.E. Consortium/LLNL at:
s: IRAK Plate: 49 Row: e Column: 5
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Eutheria; Primates; Catarrhini; Hominidae;
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/tissue_type="Lung, Spleen, feta
/clone_lib="NNH_MGC_122"
/lab_host="DH10B"
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Patent: WO 0226984-A 2 04-APR-2002;
Millennium Pharmaceuticals, Inc. (US)
Location/Qualifiers
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                                                                                         CTGTTCATCCAGTTGGATACTATGATGCACAGAAGCTCCTAGAAAAAATGGGTGGCTCAG
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Pred. No. 6.1e-313;
D; Mismatches 6;
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Halsted,C.H., Ling,E.H., Luthi-Carter,R., V
Gardner,J.M. and Coyle,J.T.
Follypoly-gamma-glutamate carboxypeptidase
Molecular characterization and relation to
carboxypeptidase II
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Rattus no
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Bzdega,T., Turi,T., Wroblewska,B.
Direct Submission
Submitted (23-OCT-1996) Biology, (
St. NW, Washington, DC 20057, USA
Location/Qualifiers
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Bzdega, T., Turi, T.,
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Molecular
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Mammalia; Eutheria;
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a rat hippocampal cDNA library
eurochem. 69 (6), 2270-2277 (1997)
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Rodentia;
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Sciurognathi; Muridae; Murinae;
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GAAVVHEUVRTFGTLKKKGWRERRTILFASWDAEEFGLLGSTEWAEEHSELLQERGVA
YINADSSIEGNYTLKVDCTPLMHSLVYNLTKELPSPDEGFEKSLYDSWKEKSPSTEF
IGMPRISKLGSGNDFEVFFQRLGIASGGARYTKHWKNNKYSYPLYHSVYETYELVEK
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KAYMISFDSLESAVNNFTDVASKFNQRLQDLDKSNPILLRILNDQLMYLERAFIDPLG
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LUGREPFYRHIIYAPSSHNKYAGESFPGIYDALFDINNKVDTSKAWREVKRQISIAAFT
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/codon_start=1
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Proc. Natl. Acad. Sci. U.S.A. 95 (6), 3215-3220 (1998)
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FYDPTFKYHLTVAQVRGAMVFELANSIVLPFDCQSYAVALKKHAETIYNISMNHPQEM
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(Naalad) mRNA,
AF513486
AF513486.1 GI:
                                                                                                                                                                                                                                                      Medicine, 780-714,
                                                                                                                                                                                                                                                             Submitted (18-MAY-2002) Department of Biochemistry, School of Medicine, Dongguk University, 707 Suk-Jang Dong, Kyungju, Kyung-Buk
                                                                                                                                                                                                                                                                                    Park, S.Y. and Lee
Direct Submission
                                                                                                                                                                                                                                                                                                                               Rattus norvegicus (Norway
Rattus norvegicus
Eukaryota; Metazoa; Chorda
Mammalia; Eutheria; Rodent
                                                                                                                                                                                                                                                                                                                      Rattus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GAGCATTTATTGATCCATTAGGGTTACCAGACAGACCTTTTTATAGGCATGTCATCTATG
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Sequence 64, Appl	_	Sequence 64, Appl		`	Sequence 96, Appl	Sequence 96, Appl	Sequence 96, Appl	•	Sequence 15, Appl	Sequence 3, Appli	Sequence 201, App	Sequence 7, Applia	Sequence 7, Appli		Sequence 74, Appl	Patent No. 5194596	Patent No. 5219739

ALIGNMENTS

Sequence 1, Application Patent No. 5538866 GENERAL INFORMATION: COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPUTER: DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/325,553 APPLICANT: Israeli, Ron S.
APPLICANT: Heston, Warren D.W.
APPLICANT: Fair, William R.
TITLE OF INVENTION: THE PROSTATE-SPECIFIC MEMBRANE ANTIGEN
NUMBER OF SEQUENCES: 38 CORRESPONDENCE ADDRESS: STREET: 30 Roc CITY: New York COUNTRY: ADDRESSEE: 10112 New York E: Cooper & Dunham 30 Rockefeller Plaza United States of America US/08325553

TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 977-9550
TELEPAX: (212) 664-0525
TELEX: 422523 COOP UI
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2653 base pairs MOLECULE TYPE: CDI HYPOTHETICAL: NO ANTI-SENSE: NO ORIGINAL SOURCE: CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UNMEER: US/07/973,337A
FILING DATE: 05 NOV 1992
ATTORNEY/AGENT INFORMATION:
NAME: The DATE: 1050 DATE: IMMEDIATE SOURCE: ORGANISM: Homo sapiens TISSUE TYPE: Carcinoma NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 17 TOPOLOGY: TYPE: nucleic acid STRANDEDNESS: double linear 1747/41426

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                                                                        Sequence 1, Application Patent No. 5935818 GENERAL INFORMATION:
APPLICANT: ISTACLI, RON S.
APPLICANT: Heston, Warren D.W.
APPLICANT: FALT, William R.
TITLE OF INVENTION: PROSTATE-SI
TITLE OF INVENTION: USES THEREO
NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham LI
STREET: 1185 Avenue of the Au
CITY: New York
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	Qy 420 CAGCANATGANTATCCTANANTCTGANTGGTGCAGAGACCCTCTCACACCAGGTATCC 1078 1111111111111111111111111111111111	######################################	uery Match 85.5%; Score 1702.6; DB 2; Length 2653; est Local Similarity 98.5%; Pred. No. 0; atches 1729; Conservative 0; Mismatches 24; Indels 2; Gaps	% - O	LENGTH: 2653 base pairs TYPE: nucleic acid STRANDEDNESS: double TOPOLOGY: linear MOLECULE TYPE: CDNA HYPOTHETICAL: NO ANTI-SENSE: NO ORIGINAL SOURCE:	IN	STATE: New York COUNTRY: United States of America ITP: 10036 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM 30 466 DX2 OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/394,152A FILING DATE: 24-FEB-95 CLASSIFICATION: 435 ATTONNEY/AGENT INFORMATION:
Qy 1620 GAGCATTTATTGATCCATTAGGGTTACCAGACAGACCTTTTATAGGCATGTCATCTATG 1679	Qy 1500 TTTCTGCAGTAAAAATTTTACAGAAATTGCTTCCAAGTTCAGCGAGAGACTCCAGGACT 1559	Db 1979 ACCITETGATTGCCAAGGTTCGAAGAGATTTTAAGAAAGTATGCATATCACTTT 1439 1380 TCCCTTTTGATTGTCGAGAGATTATGCTGTAGCTATTTAAGAAAGTATGCTGACAAATCTACA 1439 1111111111111111111111111111111111	QY 1260 ACAGTGTCTATGAAACATATGAGTTGGTGGAAAAGTTTTATGATCCAATGTTTAAAATATC 1319	OY 1140 GCAAATTGGGATCTGGAAATGATTTTGAGGTGTTCTCCAACGACTTGGAATTGCTTCAG 1199	Qy 1020 TGGTATACAACCTAACAAAAGAGCCTGAAAAAGGCCTTGAAGGCTATGAAGGCAAATCTC 1079	Qy 900 AGTGGGCAGAGGATAATTCAAGACTCCTTCAAGAGCGTTGGCTTATATTAATGCTG 959	Qy 720 TTCTGGGAGGTCACCGGGACTCATGGGTGTTTGGTGGTATTGACCCTCAGAGTGGAGCAG 779

QY 660 CGAGAATTTACAATGTGATAGGTACTCTCAGAGGAGCAGTGGAACCAGACAGA	QY 600 TTACTGGAAACTTTTCTACACAAAAAGTCAAGATGCACATCCACTCTACCAATGAAGTGA 659	OY 540 CACCACCAGATAGCAGCTGGAGAGGGAAGTCTCAAAGTGTCCTACAATGTTGGACCTGGCT 599	QY 480 CTGTTCATCCAGTTGGATACTATGATGCACAGAAGCTCCTAGAAAAATGGGTGGCTCAG 539	QY 420 CAGCAAATGAATACGCTTATAGGCATGGAATTGCAGAGGCTGTTGGTCTTCCAAGTATTC 479	QY 360 TCCAGCGTGGAAATATCCTAAATCTGAATGGTGCAGGAGACCCTCTCACACGAGGTTACC 419	35	RACCIDES 1/29; CONSELVACIVE O, MISHACCIDES 24, INCLUS 2, CEPT 240 AGGITAAAAATGCCCAGCTGGCAGGGGCCAAAGGAGTCATTCTCTACTCAAGACCCTGCTG 29	Query Match 85.5%; Score 1702.6; DB 4; Length 2653; Best Local Similarity 98.5%; Pred. No. 0; Tridels 2:	; SEO ID NO 1 ; LENGTH: 2653 ; TYPE: DNA ; ORGANIEM: Homo sapiens	; CURRENT APPLICATION NUMBER: US/08/705,477E ; CURRENT FILING DATE: 1996-08-29 ; NUMBER OF SEQ ID NOS: 1.28 ; SOFTWARE: PatentIn version 3.1	APPLICANT: Overfelli, Ouathek APPLICANT: Pinto, John TITLE OF INVENTION: PROSTATE-SPECIFIC MEN FILE REFERENCE: 1769/41426-G	GENERAL INFORMATION: APPLICANT: Israeli, Rom APPLICANT: Heston, Wan APPLICANT: Fair, Will:	RESULT 3 US-08-705-477E-1 ; Sequence 1, Application US/08705477E ; Patent No. 6569432	2639	2579 G 1978 A	Db 2519 ATTCTTTAGAGAATCCGTATTGAAATTTGTGTGTATGTCACCACAAAGAATCGTAATGG 2578 Qy 1918 GTATATTGATAAAATTTAAAATTGGTATATTTGAAATAAAGTTGAAATATTAT	2459 ATGTTGCAGCCTTCACAGTGCAGGCAGCTGCAGAGACTTTGAGTAAGTA	QY 1800 CTGTTGCAGCCTTCACAGTGCAGGCAGCTGCAGAGACTTTGAGTGAAGTGAAGCCTAAGAGG 1859
Db 23					Db 20		Qy 13	Qy 12	Qy 12	Qy 11 Db 17	Qy 10 Db 17	Оу 10 рь 16	ОУ 9 Дъ 16	ОУ 9 Дъ 15	ОУ 8 Db 14	Qy 7 Db 14	Qy 7 Db 13	Db 13
99 TTGATATISANAGCAAAGTGGACCCTTCCAAGGCCTGGGGAGAAGTGAAGAGACAGATTT	39		19 20	59 60						1140 GCAAATTGGGATCTGGAAATGATTTTGAGGTGTTCTTCCAACGACTTGGAATTGCTTCAG 1199	1080 TITATGAAAGTIGGACTAAAAAAAGTCCTTCCCCAGAGITCAGTGGCATGCCCAGGATAA 1139 	1020 TGGTATACAACCTAACAAAAGAGCTGAAAAAGCCCTGATGAAGGCTTTGAAGGCAAATCTC 1079	960 ACTCATCTATAGAAGGAAACTACACTCTGAGAGTTGATTGTACACCACTGATGTACAGCT 1019	900 AGTGGGCAGAGGATAATTCAAGACTCCTTCAAGAGCGTGGCGTGGCTTATATTAATGCTG 959 	840 GAAGAACAATTTTGTTTGCAAGCTGGGATGCAGAAGAATTTGGTCTTCTTGGTTCTACTG 899	780 CTGTTGTTCATGAAACTGTGAGGAGCTTTGGAACACTGAAAAAGGAAGG		1319 CAAGAATTTACAATGTGATAGGTACTCTCAGAGGAGCAGTGGAACCAGACAGA

660 CGAGAATTTACAATGTGATAGGTACTCTCAGAGGAGCAGTGGAACCAGACAGA	600 TTACTGGAAACTTTTCTACACAAAAAAGTCAAGATGCACATCCACTCTACCAATGAAGTGA 659	540 CACCACCAGATAGCAGCTGGAGAGGAAGTCTCAAAGTGTCCTACAATGTTGGACCTGGCT 599	480 CTGTTCATCCAGTTGGATACTATGATGCACAGAAGCTCCTAGAAAAAATGGGTGGCTCAG 539	420 CAGCAAATGAATACGCTTATAGGCATGGAAATTGCAGAGGCTGTTGGTCTTCCAAGTATTC 479	360 TCCAGCGTGGAAATATCCTAAATCTGAATGGTGCAGGAGACCCTCTCACACCAGGTTACC 419	300 ACTACTTTGCTCCTGGGGTGAAGTCCTATCCAGACGGTTGGAATCTTCCTGGAGGTGGTG 359	AGGGCCAAAGGAGTCATTCTCTACTCAGACCCTGCTG 29	Query Match 84.5%; Score 1683.4; DB 4; Length 2387; Best Local Similarity 97.8%; Pred. No. 0; Matches 1717; Conservative 0; Mismatches 36; Indels 2; Gaps 1;	LENGTH: 2387 TYPE: DNA ORGANISM: Homo sapiens 08-705-477E-100	CURRENT FILING DATE: 1996-08-29 NUMBER OF SEQ ID NOS: 128 SOFTWARE: PatentIn version 3.1 SEQ ID NO 100	APPLICANT: Pinto, John TITLE OF THE PROPERTION: PROSTATE-SPECIFIC MEMBRANE ANTIGEN AND USES THEREOF FILE REFERENCE: 1769/41426-G CURRENT APPLICATION NUMBER: US/08/705,477E	APPLICANT: Israeli, Ron S APPLICANT: Heston, Warren D.W. APPLICANT: Fair, William R. APPLICANT: Overfelli, Ouathek	3-08-705-477E-100 Sequence 100, Application US/08705477E Patent No. 6569432 GENERAL INFORMATION:	2639 AAAAAAAAAAAA 2653		GTATATTGATAAATTTTAAAATTGGTATATTTGAAATAAAGTTGAATATATATATATAAAA	1860 ATTCTTTAGAGACTCTGTATTGAATTTGTGGTGGTATGTCACTCAAAGAATAATAATAG 1917 11	
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GENERAL INFORMATION:
APPLICANT: Mincheff, Milcho S.
Foukinov, I. Dmitri
                                                                                                                                                                          Local Similarity
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APPLICATION NUMBER: US/09/164,034B
APPLICATION NUMBER: US/09/164,034B
ATTORNEY/AGENT INFORMATION:
NAME: Ramsey, William S.
REGISTRATION NUMBER: 32,715
REFERENCE/DOCKET NUMBER: bril
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MEDIUM TYPE: Diskette,
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ZIP: 21044
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CORRESPONDENCE ADDRESS:
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ATTCTTTAGAGACTCTGTATTGAATTTGTGTGGGTATGTCACTC--AAAGAATAATAATGG
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TELEFAX: (410) 992-9540
ENCE DESCRIPTION: SEQ ID NO:
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          TCCCTTTTGATTGTCGAGATTATGCTGTAGTTTTAAGAAAGTATGCTGACAAAATCTACA 1439
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; OTHER INFORMATION: n-any nucleactide
US-08-705-477E-97
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CURRENT APPLICATION NUMBER: US/08/705,477E
CURRENT FILING DATE: 1996-08-29
NUMBER OF SEQ ID NOS: 128
SOFTWARE: Patentin version 3.1
SEQ ID NO 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 97, Application US/08705477E
Patent No. 6569432
GENERAL INFORMATION:
APPLICANT: Israell, Ron S
APPLICANT: Heston, Warren D.W.
APPLICANT: Fair, William R.
APPLICANT: Overfelli, Ouathek
APPLICANT: Overfelli, Ouathek
APPLICANT: Pinto, John
TITLE OF INVENTION: PROSTATE-SPECIFIC MEMBRANE ANTIGEN AND USES THEREOF
Sequence 96, Application US/08705477E Patent No. 6569432 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
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Pred. No. 3.4e-50;
0; Mismatches 9;
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APPLICANT: Heston, Warren D.W.
APPLICANT: Heston, Walliam R.
APPLICANT: Fair, William R.
APPLICANT: Overfelli, Ouathek
APPLICANT: Overfelli, Ouathek
APPLICANT: Pinto, John
TITLE OF INVENTION: PROSTATE-SPECIFIC MEMBRANE ANTIGEN AND USES THEREOF
FILE REFERENCE: 1769/41426-G
CURRENT APPLICATION NUMBER: US/08/705,477E
CURRENT APPLICATION NUMBER: US/08/705,477E
CURRENT FILING DATE: 1996-08-29
NUMBER OF SEQ ID NOS: 128
SOFTWARE: Patentin version 3.1
SEQ ID NO 96
LENGTH: 783
TWOPE: TAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Patent No. 5935818 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 45,
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Best Local :
                                                                                                                        COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM 330 466 DX2
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/394,152A
FILING DATE: 24-FEB-95
CLASSIFICATION: 435
             REFERENCE/DOCKET NUMBER: 41
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEPHAX: (212) 391-0525
                                                                         ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Heston, Warren D.W. APPLICANT: Fair, William R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                     CITY: New York
STATE: New York
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1185 Avenue of the Americas
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Pred. No. 3.4e-50;
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APPLICANT: Xu, Jiangchun

APPLICANT: Dillon, Davin C.

APPLICANT: Mitcham, Jennifer L.

APPLICANT: Harlocker, Susan Louise

APPLICANT: Harlocker, Susan Louise

APPLICANT: Reed, Steven G.

APPLICANT: Reade, Steven G.

APPLICANT: Realos, Michael

APPLICANT: Fanger, Gary

APPLICANT: Retter, Mark

APPLICANT: Bolk, John

APPLICANT: Day, Craig

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND

TITLE OF INVENTION: DIACMOSIS OF PROSTATE CANCER

FILE REFERENCE: 201011.47C9

CURRENT APPLICATION NUMBER: US/09/439,313

CURRENT FILING DATE: 1999-11-12
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; CLONE: Prostate Specific Membrane Antigen
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                                                         ; TYPE: DNA; ORGANISM: Homo sapiens US-09-439-313-454
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US-09-439-313-454/c
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Best Local S
Matches 256
                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 454, Application US/09439313 Patent No. 6329505
                                                                                                   NUMBER OF SEQ ID NOS: 575
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 454
LENGTH: 231
                           Query Match
 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 893 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: peptide HYPOTHETICAL: NO ANTI-SENSE: NO
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hes 256;
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             Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               156 TAATGAGAAAAAGGTTGAAGATAAAGTTCTGGTACTCATTTAAGTGTAATATTAAAAATT
222;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AGGTTAAAAATGCCCAGCTGGCAGGGGCCAAAGGAG 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GATATTACCGAATCTGGAACAACCAATTTAAAATAAGGAAAAAAAGACACTGTGTAAACT
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Conservative
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E: Carcinoma
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92.8%;
               11.1%;
98.7%;
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 0,;
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Pred. No. 8.6e-50;
               Score 220.2; DB Pred. No. 2.9e-49
 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18;
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                             4.
                               Length
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APPLICANT: Dillon, Louise
APPLICANT: Harlocker, Susan Louise
APPLICANT: Jiang, Yuqui
APPLICANT: Jiang, Yuqui
APPLICANT: Xu, Jiangchun
APPLICANT: Mitcham, Jennifer Lynn
ITILE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIA
ITILE OF INVENTION: OF PROSTATE CANCER AND METHODS FOR
ITILE REFERENCE: 210121.42708
CURRENT APPLICATION NUMBER: US/09/352,616A
CURRENT FILING DATE: 1999-07-13
MINMBER OF SEQ ID NOS: 472
MINMBER OF SEQ ID NOS: 472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 10
US-09-352-616A-454/c
; Sequence 454, Application US/09352616A
; Patent No. 6395278
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                                                                                                      ; Sequence 27, Application
; Patent No. 5538866
                                                                                                                                RESULT 11
US-08-325-553-27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID NO 454
LENGTH: 231
TYPE: DNA
ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                       Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                         GENERAL INFORMATION:
         APPLICANT: Israeli, Ron S.
APPLICANT: Heston, Warren D.W.
APPLICANT: Fair, William R.
TITLE OF INVENTION: THE PROSTATE-SPECIFIC
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                     Local
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                                                                                                                                                                                                                                                      TGAGTGGGCAGAGGATAATTCAAGACTCCTTCAAGAGGCGTGGCGTGGCTTATATTAATGC 957
                                                                                                                                                                                       TGACTCATCTATAGAAGGAAACTACACTCTGAGAGTTGATTGTAC
                                                                                                                                                                                                                                           TGAGTGAGCAGAGGAGATTCAAGACTCCTTCAAGAGCGTGGCGTGGCTTATATTAATGC
                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
Cooper & Dunham
                                                                                                                                                                                                                                                                                                                                                                                                                     11.1%;
98.7%;
                                                                                                                     US/08325553
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Pred. No. 2.9e-49;
0; Mismatches 3
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; ANTI-SENSE: US-08-325-553-27
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Best Local Similarity
Matches 370; Conserv
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/973,337A
FILING DATE: 05 NOV 1992
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 1747/41426
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 977-9550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 780 base pairs
TYPE: nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEX: (212) 664-0525
TELEX: 422523 COOP UI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                              628 CAAGATGCACATCCACTCTACCAATGAAGTGACGAGAATTTACAATGTGATAGGTACTCT
                                                                                                                                                                                                                                                                                                                                                                                            211 GATCCANNNTTCCTGTAAGGTNNGACNNAACAAAGCAGGAGANNNNGCCAGANTAATGGT
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GGATGCAGAAGAATTTGGTCTTCTTGGTTCTACTGAGTGGGCAGAGGATAATTCAAGACT
                                           CTCAGACATAGTGAAAAACGAGGGCTACAAACCGAGGCGAAGCATCATCTTTGCTAGCTG
                                                                                    CCCAGGAGTGGCTAAAGCTGGCACTGGAACTGCTATATTGTTGGAACTTGCCCGTGTGAT
                                                                                                                                                                       GTTTGGTGGTATTGACCCTCAGAGTGGAGCAGCTGTTGTTCATGAAACTGTGAG---GAG
                                                                                                                                                                                                                  CCAGGGATTTGAAGAACCTGATCGGTATGTTGTGATTGGAGCCCCAGAGAGACTCCTGGGG
                                                                                                                                                                                                                                                         CAGAGGAGCAGTGGAACCAGACAGATATGTCATTCTGGGAGGTCACCGGGACTCATGGGT
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51.6%;
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Pred. No. 1.8e-31;
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                                                                                                                 Matches
                                                                                                                                           Query Match
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                                                                                                                                                                                                                                                                                                      TELEFAX: (212) 391-0525 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                    MOLECULE HYPOTHETICAL: N
                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 41
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
COMPUTER: IBM 330 46
                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                MOLECULE TYPE:
                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Fair, William R.
                                                                                                                               Local Similarity
                                                                                                                                                                                                                               TOPOLOGY:
                                                                                                                                                                                                                                             STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                  TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: FILING DATE: 24-FE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM 330 466 DX2
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET:
                                                                                                                                                                                                                                                                                                                                                                                             NAME: White,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE:
                                                                                                                                                                                                                                                                          LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1043 CTGAAAAGCCCTGATGAAGGCTTTGAAGGCAAATCTCTTTATGAAAGTTGGACTAAA 1099
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                                                                                   388 TGGTGCAGGAGACCCTCTCACCAGGTTACCCAGCAAATGAATACGCTTATAGGCATGG
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Heston, Warren
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51.6%;
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Pred. No. 1.8e-31;
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Sequence 27, Application US/08705477E

Patent No. 6569432

GENERAL INFORMATION:

APPLICANT: Israeli, Ron S
APPLICANT: Heston, Warren D.W.

APPLICANT: Fair, William R.

APPLICANT: Pinto, John

TITLE OF INVENTION: PROSTATE SPECIFIC MEMBRANE ANTIGEN AND FILE REFERENCE: 1769/41426-G

CURRENT APPLICATION NUMBER: US/08/705,477E

CURRENT FILING DATE: 1996-08-29

NUMBER OF SEQ ID NOS: 128

SOFTMARE: Patentin version 3.1

SEQ ID NO 27

LENGTH: 780
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US-08-705-477E-27
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NAME/KEY: misc_feature LOCATION: (196)..(197) OTHER INFORMATION: n-any
                                                                                                                                       NAME/KEY: misc_feature LOCATION: (82)..(84) OTHER INFORMATION: n-any
                                                                                   NAME/KEY: misc_feature LOCATION: (193)..(193)
                                                       FEATURE:
                                                                  OTHER INFORMATION: n=any
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; LOCATION: (721)...(724)
; OTHER INFORMATION: n=ar
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NAME/KEY: misc_feature
'COATION: (217)..(219)
'COATION: (217)...
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OTHER INFORMATION: n=a
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Similarity 51.6%;
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                                  CCTTCAAGAGCGTGGCGTGGCTTATATTAATGCT--GACTCATCTATAGAAGGAAACTAC
                                                                    GAGTGCAGGAGACTACGGAGCTGTGGGTGCTACTGAATGGCTGGAGGGGTACTCTGCCAT
                                                                                      GGATGCAGAAGAATTTGGTCTTTGGTTCTACTGAGTGGGCAGAGGATAATTCAAGACT
                                                                                                                                         CTCAGACATAGTGAAAAACGAGGGGTACAAACCGAGGCGAAGCATCATCTTTGCTAGCTG
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Pred. No. 1.8e-31;
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US-08-325-553-28
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                                                                                                                                                                                  Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 28,
                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 1747
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 977-9550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                               TOPOLOGY: Li
                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 660 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/973,337A
FILING DATE: 05 NOV 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                   HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LILLE OF INVENTION: THE PROSTATE-SPECIFIC MEMBRANE ANTIGEN NUMBER OF SEQUENCES: 38
                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (212) 664-0525
TELEX: 422523 COOP UI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0
                                                                                                                                                                                                                                                                                                                STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
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                  740 TCATGGGTGTTTGGTGGTATTGACCCTCAGAGT-GGAGCAGCTGTTGTTCATGAAACTGT
                                                           149 GGCGTTATTAAAGGCTATGAGGAACCAGACCGCTACATTGTAGTAGGAGCCCAGAGAGAC
                                                                                                                                                620 CAAAAAGTCAAGATGCACATCCACTCTACCAATGAAGTGACGAGAATTTACAATGTGATA 679
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                                                                                                                                                                                                                                                                                                                         nucleic acid
                                                                                                                   GGTACTCTCAGAGGAGCAGTGGAACCAGACAGATATGTCATTCTGGGAGGTCACCGGGAC
    GCTTGGGGCCCTGGTNGTTGCGAAGTCCAGTGTGGGAACAGGTCTTNCTGTTGAAACTTG
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Heston, Warren D.W.
Fair, William R.
VENTTON: ....
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                                                                                                                                                                            Score 85.8; DI
Pred. No. 2.6e:
0; Mismatches
                                                                                                                                                                               0;
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                                                                                                                                                                            ; DB 1;
2.6e-13;
hes 218;
                                                                                                                                                                                                         Length 660;
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                                                          208
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US-08-394-152A-28
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                                              US-08-394-152A-28
Query Match
Best Local Similarity
                                                             HYPOTHETICAL:
ANTI-SENSE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
                                                                                                     TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
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Sequence 28, Application US/08394152A Patent No. 5935818
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                                                                                                            TELEPHONE: (212) 278-0
TELEFAX: (212) 391-052
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM 330 466 DX2
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Heston, Warren D.W.
APPLICANT: Fair, William R.
TITLE OF INVENTION: PROSTATE-SPE
TITLE OF INVENTION: USES THEREOF
NUMBER OF SEQUENCES: 48
                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
MOLECULE TYPE:
                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 41 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: FILING DATE: 24-FEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 1185 A
CITY: New York
                                             STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
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                                                                 nucleic acid
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1185 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                United States of America
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N: 435
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4.3%;

Score Pred.

85.8; DB 2; No. 2.6e-13;

Length 660;

CAAAAAGTCAAGATGCACTCCACTCTACCAATGAAGTGACGAGAATTTACAATGTGAAT [267; Conservative 0; Mismatches 218; Indels 10; Gaps 5 620 CAAAAAGTCAAGATGCACATCCACTCTACCAATGAAGTGACAATTTACAATGTGATA 679
א מים אַאַ מים אַאַ	Indels 10 CGAGAATTTACAI CAAGAATACTTAI CTTGGGAGGTCJ TTCTGGGAGGTCCL TAGTAGGACCCL TAGTAGGACCCL GCTGTTGTTCATC GGTCTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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seq length: 2000000000
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1992
1 agcaaatactcacta
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: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
0: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
0: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
1: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
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4: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
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6: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*
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Copyright (c) 1993 - 2003 Compu
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/cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
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/cgn2_6/ptodata/1/pubpna/PCT_1
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Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARI

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Result No.	Score	Query Match	Length	DB	ID	Description
1	1702.6	85.5	2653	10	US-09-969-708-536	Sequence 536, App
2	1702.6	85.5	2653	12	US-09-873-319-451	451,
ω	٠	85.5	2653	12	US-09-960-706-716	716,
4	1702.6	85.5	2653	12	US-10-210-120-5	5 A
5	1702.6	85.5	2653	14	US-10-094-699-2	N.
on.	1702.6	85.5	2653	14	US-10-205-823-131	131
7	٠	84.7	2558	10	US-09-978-295A-617	617,
8	1687.2	84.7	2558	10	US-09-978-697-617	Sequence 617, App
9	•	84.7	2558	10	US-09-978-192A-617	•
10		84.7	2558	10	US-09-999-832A-617	617,
11	1687.2	84.7	2558	11	US-09-978-189-617	•
12		84.7	2558	11	US-09-978-608A-617	617,
13	1687.2	84.7	2558	11	US-09-978-585A-617	617,
14	1687.2	84.7	2558	11	US-09-978-191A-617	617,
15	1687.2	84.7	2558	11	US-09-978-403A-617	617,
16	1687.2	84.7	2558	1	US-09-978-564A-617	

45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18
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RESULT 1 US-09-969-708-536

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CURRENT FILING DATE: 2001-10-03
PRIOR APPLICATION NUMBER: US/60/237,606
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: US/60/237,608
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: US/60/237,425
PRIOR APPLICATION NUMBER: US/60/237,425
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Augustus, Meena
APPLICANT: Augustus, Meena
TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Sign
TITLE OF INVENTION: Sets
FILE REFERENCE: 689290-70
                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 1729; Conserv
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SOFTWARE: PatentIn version 3.0
SEQ ID NO 536
LENGTH: 2653
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TCCAGCGTGGAAATATCCTAAATCTGAATGGTGCAGGAGACCCTCTCACACCCAGGTTACC
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Pred. No. 0;
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APPLICANT: Getzenberg, Robert H.
APPLICANT: Waga, Iwao
APPLICANT: Yamamoto, Jun
TITLE OF INVENTION: Identifying Drugs for and
TITLE OF INVENTION: Identifying Drugs for and
TITLE OF INVENTION: Hyperplasia Using Gene Ex-
FILE REFERENCE: 44921-509-US
CURRENT APPLICATION NUMBER: US/09/873,319A
CURRENT FILING DATE: 2001-06-05
EARLIER APPLICATION NUMBER: US 60/223,323
EARLIER FILING DATE: 2000-08-07
NUMBER OF SEQ ID NOS: 755
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 451
LENGTH: 2653
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US-09-873-319-451
US-09-873-319-451, Application US/09873319A
Sequence 451, Application US/09873319A
                                                                                                    ; OTHER INFORMATION: US-09-873-319-451
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publication No. US200
GENERAL INFORMATION;
APPLICANT: Munger, W
APPLICANT: Kulkarni,
                                                Query Match
Best Local S
Matches 1729
                                                                                                                            TYPE: DNA
ORGANISM: Homo :
FEATURE:
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Kulkarni, Prakash
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TITLE OF INVENTION: Identifying Drugs for and Dia TITLE OF INVENTION: Gene Expression Profiles FILE REFERENCE: 4491-5029-01US

CURRENT APPLICATION NUMBER: US/09/960,706

CURRENT FILING DATE: 2001-09-24

PRIOR APPLICATION NUMBER: 60/23,323

PRIOR FILING DATE: 2000-08-07

PRIOR APPLICATION NUMBER: 09/873,319

PRIOR APPLICATION NUMBER: 09/873,319

PRIOR FILING DATE: 2001-06-05

NUMBER OF SEQ ID NOS: 1124

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 716

LENGTH: 2653

TYPE: DNA

ORGANIEM: Homo sapiens
                                                                                                                                                                                                                                                                                                                           Sequence 716, Application US/09960706
Publication No. US20030134280A1
GENERAL INFORMATION:
APPLICANT: Munger, William E.
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US-10-210-120-5
                                                                                                                                                                                                                                                            Sequence 5, Application US/10210120 Publication No. US20030175736A1 GENERAL INFORMATION:
                                                                            SOFTWARE: PatentIn
SEQ ID NO 5
                                                                                                                                  APPLICANT: Sreekumar, Arun
TITLE OF INVENTION: Expression Profile of
FILE REFERENCE: UM-07221
CURRENT APPLICATION NUMBER: US/10/210,120
CURRENT FILING DATE: 2002-08-01
PRIOR APPLICATION NUMBER: US 60/309,581
PRIOR FILING DATE: 2001-08-02
PRIOR FILING DATE: 2001-08-02
Query Match
                                                                                                    PRIOR APPLICATION NUMBER: US 60/309,581
PRIOR FILING DATE: 2001-08-02
PRIOR APPLICATION NUMBER: US 60/334,468
PRIOR FILING DATE: 2001-11-15
NUMBER OF SEQ ID NOS: 123
                                                                                                                                                                                                                                  APPLICANT: Chinnaiyan, Arul M. APPLICANT: Rubin, Mark A.
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     Sequence 2, Application US/10094699
PUBLICATION NO. US20030046714A1
GENERAL INFORMATION:
APPLICANT: SIMARD, John, J.L.
APPLICANT: DIAMOND, David, C.
TITLE OF INVENTION: ANTI-NEOVASCULATURE PREP
TITLE OF INVENTION: CANCER
FILE REFERENCE: CTLIMM.015A
CURRENT FAPLICATION NUMBER: US/10/094,699
CURRENT FILING DATE: 2002-06-21
PRIOR APPLICATION NUMBER: US 60/274,063
PRIOR FILING DATE: 2001-03-07
NUMBER OF SEQ ID NOS: 109
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 2653
TYPE: DNA
ORGANISM: Homo sapien
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US-10-094-699-2
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                             GCAGAGCACGGTATACTAAAAATTGGGAAACAAACAAATTCAGCGGCTATCCACTGTATC
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US-10-205-823-131
Sequence 131, Applicat
Publication No. US200:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Schlegel,
APPLICANT: Monahan,
APPLICANT: Endege, Wilson O.
APPLICANT: Gannavarapu, Manjula
APPLICANT: Gorbatcheva, Bella
APPLICANT: Hoersch, Sebastian
APPLICANT: Hoersch, Sebastian
APPLICANT: Wonsey, Angela M.
APPLICANT: Glatt, Karen
APPLICANT: Jao, Xumei
APPLICANT: Anderson, Dustin
APPLICANT: Anderson, Dustin
APPLICANT: Anderson, Dustin
TITLE OF INVENTION: METHODS FOR IDENTIFICATION, AS
TITLE OF INVENTION: THERAPY OF PROSTATE CANCER
FILE REFERENCE: MRI-044
CURRENT APPLICATION NUMBER: US/10/205,823
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Monahan, John E.
Endege, Wilson O.
Gannavarapu, Manjula
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                                 ASSESSMENT,
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Qy 960 actcatctatagaaggaaactacactctgagagttgatacaccactgatgtacacct 1019 	QY 900 AGTGGGCAGAGGATAATTCAAGACTCCTTCAAGAGCGTGGCGTGGCTTATATATGCTG 959	OY 840 GAAGAACAATTTTGTTTGCAAGCTGGGATGCAGAAGAATTTGGTCTTCTTGGTTCTACTG 899	QY 780 CTGTTGTTCATGAAACTGTGAGGAGCTTTGGAACACTGAAAAAGGAAGG	Qy 720 TTCTGGGAGGTCACCGGGACTCATGGGTGTTTGGTGGTATTGACCCTCAGAGTGGAGCAG 779	Qy 660 CGAGAATTTACAATGTGATAGGTACTCTCAGAGGAGCAGTGGAACCAGACAGA	Qy 600 TTACTGGAAACTTTTCTACACAAAAAGTCAAGATGCACATCCACTCTACCAATGAAGTGA 659	QY 540 CACCACAGATAGCAGCTGGAGAGGAAGTCTCAAAGTGTCCTACAATGTTGGACCTGGCT 599	OY 480 CTGTTCATCCAGTTGGATACTATGATGCACAGAAGCTCCTAGAAAAAATGGGTGGCTCAG 539	QY 420 CAGCAAATGAATACGCTTATAGGCATGGAATTGCAGAGGCTGTTGGTCTTCCAAGTATTC 479	OY 360 TCCAGCGTGGAAATATCCTAAATCTGAATGGTGCAGGAGACCCTCTCACACCAGGTTACC 419	QY 300 ACTACTTTGCTCCTGGGGTGAAGTCCTATCCAGACGGTTGGAATCTTCCTGGAGGTGGTG 359	QY 240 AGGTTAAAAATGCCCAGCTGGCAGGGGCCAAAGGAGTCATTCTCTACTCAGACCCTGCTG 299	Ma Be	ENGTH: TPE: DN RGANISM	PRIOR FILING DATE: 2002-03-05 NUMBER OF SEQ ID NOS: 455 SOFTWARE: FastSEQ for Windows Vers SEO ID NO 131	PRIOR FILING DATE: 2001-09-25 PRIOR APPLICATION NUMBER: 60/341, PRIOR FILING DATE: 2001-12-12 PRIOR APPLICATION NUMBER: 60/362,	PRIOR PRIOR PRIOR	; CURRENT FILING DATE: 2002-07-25; PRIOR APPLICATION NUMBER: 60/307,982
RESULT 7 US-09-978-295A-617	Db 2639 AAAAAAAAAAAAAA 2653	1910 STATATTGATAAATT	1600 ATTCTTIAGAGACICTGIATIGAATITIGTGIGGAGIGICACIC - AAAGAATAAITAGG 	1800 CTGTTGCAGCCTTCACAGTGCAGGCACCTGCAAGAAGACTTGAATGAA	1740 TIGATATIGAAGCAAGTIGGACCCTTCCAAGGCCTGGGGAGATGTGAAGACACAGATTT. 179	1680 CTCCAAGCACCACAACAACTATGCAGGGGACTCATTCCCAGGAATTTATGATGCTCTGT	Oy 1620 GAGCATTTATIGATICCATTAGGGTTACCAGACAGCCTTTTATIAGGCATGTCATCTATG 1679	1300 IISKORANSKORANSKORANISTI ISTI INSKRIJANISTANISTI KORSTITIONSKI ISTI ISTORIJA I STATI I ST	1500 TTTCTGCAGTAAAAATTTTTACAAAATTGCTTCCAAGTTCAGGGGAGACTCCAGGACT	1440 ATATTTCTATGAAACATCCACAGGAAATGAAGACATACAGTTTATCATTTGATTCACTTT 149	Qy 1380 TCCCTTTGATTGTCGAGATTATGCTGTAGTTTTAAGAAAGTATGCTGACAAAATCTACA 1439	ACCTCACTGTGGCCCAGGTTCGAGGAGGGATGGTGTTTGAGCTAGCCAATTCCATAGTGC	1260 ACAGTGTCTATGAAACATATGAGTTGGTGGAAAAGTTTTATGATCCAATGTTTAAAATATC	Oy 1200 GCAGAGCACGGTATACTAAAAATTGGGAAACAAACTAACAGCGGCTATCCACTGTATC 1259	QY 1140 GCAAATTGGGATCTGGAAATGATTTTGAGGTGTTCTTCCAACGACTTGGAATTGCTTCAG 1199	QY 1080 TTTATGAAAGTTGGACTAAAAAAGTCCTTCCCCAGAGTTCAGTGGCATGCCCAGGATAA 1139	Qy 1020 TGGTATACAACCTAACAAAAGAGCTGAAAAGCCCTGATGAAGGCTTTGAAGGCAAATCTC 1079	Db 1619 ACTCATCTATAGAAGGAAACTACACTCTGAGAGTTGATTGTACACCGCTGATGTACAGCT 1678

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Sequence
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APPLICANT: Baker Kevin P
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Sequence 617, A
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmer
TITLE OF INVENTION: Acids Encoding the:
TITLE REFERENCE: P2630P1C27
CURRENT APPLICATION NUMBER: U5/09/978,69
CURRENT FILING DATE: 2001-10-16
PRIOR APPLICATION NUMBER: 09/91858
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR APPLICATION NUMBER: 60/062249
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
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APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoli
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Gurney, Austin L.
Hillan, Kenneth J
Kljavin, Ivar J.
Kuo, Sophia S.
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                                                                                                                                        Roy, Margaret Ann
Shelton, David L.
Stewart, Timothy A.
Tumas, Daniel
Williams, P. Mickey
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Godowski, Paul J
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Botstein, David
                                                                                                                                                                                                                        Napier, Mary A.
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APPLICATION NUMBER: 60/077791 FILING DATE: 1998-0 APPLICATION NUMBER: APPLICATION NUMBER: 60/066364 FILING DATE: 1997-11-21 APPLICATION NUMBER: 60/077450 APPLICATION APPLICATION NUMBER: 60/ FILING DATE: 1998-04-08 APPLICATION NUMBER: 60/ FILING DATE: 1998-04-08 FILING DATE: 1998-03-25 APPLICATION NUMBER: 60/079656 FILING DATE: APPLICATION NUMBER: FILING DATE: APPLICATION NUMBER: APPLICATION NUMBER: 6 FILING DATE: 1997-11-APPLICATION NUMBER: APPLICATION NUMBER: APPLICATION NUMBER: NUMBER: 60/1: 1998-04-15 NUMBER: NUMBER: NUMBER: 60/081071 момвек: 60/079689 1998-03-27 1998-04-08 1998-03-11 1998-03-11 1998-03-10 1998-03-26 1998-03-1998-03-20 1998-03-13 1998-03-1998-03-1998-04-09 1998-03-20 1998-03-20 1998-03-27 UMBER: 60/079663 1998-03-27 998-04-09 60/077649 60/077632 60/079728 60/078910 60/078936 60/078886 60/080165 60/079923 60/079294 60/077641 60/065311 60/081955 60/081229 60/081203 60/081195 60/081049 60/081070 60/080334 60/080333 60/080328 60/080327 60/080194 60/080107 60/080105 60/079920 60/079786 60/079664 60/078939 20

Indels Length

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OR FILING DATE: 1998-04-29
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OR APPLICATION NUMBER: 60/082569
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RESULT 9
US-09-978-192A-617
Sequence 617, Application US
Sequence 617, Application US
Patent No. US20020177553A1
GENERAL INFORMATION:
APPLICANT: Baker Kevin P.
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napole
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APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrar
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630P1C9
CURRENT APPLICATION NUMBER: US/09/978,192A
CURRENT FILING DATE: 2001-10-15
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OR FILING DATE: 1998-03-20
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OR APPLICATION NUMBER: 60/078939
OR FILING DATE: 1998-03-20
OR APPLICATION NUMBER: 60/079294
OR FILING DATE: 1998-03-25
OR APPLICATION NUMBER: 60/079656
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OR APPLICATION NUMBER: 60/079664
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OR APPLICATION NUMBER: 60/079689
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OR APPLICATION NUMBER: 60/079663
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OR FILING DATE: 2001-07-30
OR APPLICATION NUMBER: 60/062250
OR FILING DATE: 1997-10-17
OR APPLICATION NUMBER: 60/064249
OR FILING DATE: 1997-11-03
OR APPLICATION NUMBER: 60/065311
OR APPLICATION NUMBER: 60/066364
OR FILING DATE: 1997-11-13
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DR APPLICATION NUMBER: 60/077791

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DR APPLICATION NUMBER: 60/078004

DR APPLICATION NUMBER: 60/078086

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Kljavin, Ivar J.
Kuo, Sophia S.
Napier, Mary A.
Pan, James;
Paoni, Nicholas F
Roy, Margaret Ann
Shelton, David L.
Stewart, Timothy
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Fong, Shern
Gao, Wei-Qi
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Godowski, Paul J.
Grimaldi, J. Christopher
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OR APPLICATION NUMBER: 60/082797
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OR APPLICATION NUMBER: 60/083392
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OR APPLICATION NUMBER: 60/080333

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OR APPLICATION NUMBER: 60/080334

OR FILING DATE: 1998-04-01

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GENERAL INFORMATION.

APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Besterin, David
APPLICANT: Destetin, David
APPLICANT: Destetin, David
APPLICANT: Desnoyers, Luc
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APPLICANT: Eaton, Dan
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APPLICANT: Feirara, Napoleon
APPLICANT: Gac, Wei-Qiang
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APPLICANT: Gerier, Hanspeter
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APPLICANT: Hillan, Kenneth J
APPLICANT: Kijavin, Ivar J
APPLICANT: Kijavin, Ivar J
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APPLICANT: Napier, Mary A.
APPLICANT: Napier, Mary A.
APPLICANT: Roy, Margaret Ann
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
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APPLICANT: Williams, P. Mickey
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PRIOR APPLICATION NUMBER: 60/062311
PRIOR APPLICATION NUMBER: 60/063311
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RESULT 11

US-09-78-189-617
; Sequence 617, Application US/09978189
; Publication No. US20030004102A1
; GENERAL INFORMATION:
APPLICANT: Ashkenzai, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botsetin, David
APPLICANT: Beston, Dan
APPLICANT: Eaton, Dan
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerber, Mary E.
APPLICANT: Godowski, Paul J.
APPLICANT: Godowski, Paul J.
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.

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CURRENT FILING DATE: US/09/978.
CURRENT FILING DATE: 2001-01-0-15
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR PAPPLICATION NUMBER: 60/062250
PRIOR APPLICATION NUMBER: 60/062250
PRIOR APPLICATION NUMBER: 60/064249
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR FILING DATE: 1997-11-13
PRIOR PRIOR DATE: 1997-11-21
PRIOR APPLICATION NUMBER: 60/06364
PRIOR APPLICATION NUMBER: 60/077450
PRIOR APPLICATION NUMBER: 60/077632
PRIOR APPLICATION NUMBER: 60/077632
PRIOR APPLICATION NUMBER: 60/077641
PRIOR APPLICATION NUMBER: 60/077641
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TITLE OF INVENTION: Secreted and Tra
TITLE OF INVENTION: Acids Encoding
FILE REFERENCE: P2630P1C7
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DR FILING DATE: 1998-03-12
DR APPLICATION NUMBER: 60/078004
DR FILING DATE: 1998-03-13
OR APPLICATION NUMBER: 60/078886
DR FILING DATE: 1998-03-20
OR APPLICATION NUMBER: 60/078936
OR FILING DATE: 1998-03-20
OR APPLICATION NUMBER: 60/078939
OR FILING DATE: 1998-03-20
OR APPLICATION NUMBER: 60/079294
OR FILING DATE: 1998-03-25
OR APPLICATION NUMBER: 60/079294
OR FILING DATE: 1998-03-26
OR APPLICATION NUMBER: 60/079656
OR FILING DATE: 1998-03-26
OR APPLICATION NUMBER: 60/079664
OR APPLICATION NUMBER: 60/079664
OR FILING DATE: 1998-03-27
OR APPLICATION NUMBER: 60/079663
OR FILING DATE: 1998-03-27
OR APPLICATION NUMBER: 60/079663
OR FILING DATE: 1998-03-27
OR APPLICATION NUMBER: 60/079728
OR FILING DATE: 1998-03-27
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R FILING DATE: 1998-04-22

DR APPLICATION NUMBER: 60/082797

DR FILING DATE: 1998-04-22

DR APPLICATION NUMBER: 60/082796

OR FILING DATE: 1998-04-23

DR APPLICATION NUMBER: 60/08336

DR APPLICATION NUMBER: 60/08332

DR APPLICATION NUMBER: 60/083322

DR APPLICATION NUMBER: 60/083322

DR APPLICATION NUMBER: 60/083392

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OR FILING DATE: 1998-04-01
OR APPLICATION NUMBER: 60/081070
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OR APPLICATION NUMBER: 60/081049
OR APPLICATION NUMBER: 60/081071
OR FILING DATE: 1998-04-08
OR APPLICATION NUMBER: 60/081195
OR APPLICATION NUMBER: 60/081203
OR FILING DATE: 1998-04-09
OR APPLICATION NUMBER: 60/081203
OR FILING DATE: 1998-04-09
OR APPLICATION NUMBER: 60/081229
OR APPLICATION NUMBER: 60/08125
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OR APPLICATION NUMBER: 60/081817
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OR FILING DATE: 1998-04-15
OR APPLICATION NUMBER: 60/082568
OR FILING DATE: 1998-04-21
OR APPLICATION NUMBER: 60/082569
OR FILING DATE: 1998-04-21
OR APPLICATION NUMBER: 60/082704
OR FILING DATE: 1998-04-22
OR APPLICATION NUMBER: 60/082804
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DR APPLICATION NUMBER: 60/084640
DR FILING DATE: 1998-05-07
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ОУ ОУ	Qy Db	Qy	Qу Db	Qy	Qy	Qy	Оy	Qy	Qy Db	Qу	Qy	Qy	Qy	Qy	Qy Db	Фр	Qy Db
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Publication No. US20033049633Al
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin p.
APPLICANT: Bestein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Ferrara, Napoleon
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Godowski, Paul J.
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Goddwski, Paul J.
APPLICANT: Godwski, Paul J.
APPLICANT: Godwski, Paul J.
APPLICANT: Godwski, Faul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Gurney, Austin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Paoni, Nicholas F.
APPLICANT: Paoni, Nicholas F.
APPLICANT: Paoni, Nicholas F.
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US-09-978-585A-617
                                                           APPLICANT: Shelton, David I
APPLICANT: Stewart, Timothy
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mic
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted
TITLE OF INVENTION: ACIDS E
FILE REFERENCE: P3630P1C15
Prior Application removed SEQ ID NO 617 LENGTH: 2558
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                                         CURRENT APPLICATION NUMBER: US/09/978 CURRENT FILING DATE: 2001-10-16
                              NUMBER OF SEQ ID NOS: 624
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Gurney, Austin L.
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Stewart, Timothy A.
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 GCAGAGCACGGTATACTAAAAATTGGGAAACAAACAAATTCAGCGGCTATCCACTGTATC
                                 GCAAATTGGGATCTGGAAATGATTTTGAGGTGTTCTTCCAACGACTTGGAATTGCTTCAG
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                                                                                                                                                                                                                                 INFORMATION:
  Gerber, Hanspeter
Gerritsen, Mary E.
Goddard, Audrey
Godowski, Paul J.
Grimaldi, J. Christopher
Gurney, Austin L.
Hillan, Kenneth J
                                                                                                                                                                                                                   Ashkenazi,
                                                                                                                                                                                                                                           7, Application US/09978191A No. US20030050239A1
                                                                                                                                                                                                                                                                                                                            CTGTTGCAGCCTTCACAGTGCAGGCAGCTGCAGAGACTTTGAGTGAAGTAGCCTAAGAGG 1859
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                                                                                                   Gao,
                                                                                                              Fong,
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                                                                                                                                                                       Botstein, David
Desnoyers, Luc
                                                                                                                                                          Eaton,
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                                                                                                   Wei-Qiang
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f, Ellen
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PRIOR ETLING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR ETLING DATE: 1997-10-17
PRIOR ETLING DATE: 1997-11-03
PRIOR PILING DATE: 1997-11-03
PRIOR FILING DATE: 1997-11-13
PRIOR FILING DATE: 1997-11-13
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: 60/06364
PRIOR APPLICATION NUMBER: 60/077450
PRIOR APPLICATION NUMBER: 60/077450
PRIOR PILING DATE: 1998-03-10
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PRIOR APPLICATION NUMBER: 60/077632
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TITLE OF INVENTION: Secreted and Transmembrane
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630P1C4
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Shelton, David L.
Stewart, Timothy A.
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Kuo, Sophia S.
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                         CACCACCAGATAGCAGCTGGAGAGGAAGTCTCAAAGTGCCCTACAATGTTGGACCTGGCT
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APPLICATION NUMBER: 60/1 FILING DATE: 1998-04-08

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APPLICATION NUMBER:

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APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630P1C17
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Shelton, David L.
Stewart, Timothy A.
Tumas, Daniel
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Botstein, David
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Gurney, Austin L.
Hillan, Kenneth J
Kljavin, Ivar J.
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Gerber, Hanspeter
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Search completed: October 4, 2003, 23:20:02 Job time: 654 secs THIS PAGE BLANK (USPTO)

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US-09-978-189-618

US-09-978-585A-618

US-09-978-191A-618

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ALIGNMENTS

RESULT 1 US-09-822-827-944

Sequence 944, Application US/09822827 Patent No. US20020081680A1 GENERAL INFORMATION:

APPLICANT: Xu, Jiangchun
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.534C1
CURRENT APPLICATION NUMBER: US/09/822,827
CURRENT FILING DATE: 2001-03-28
NUMBER OF SEQ ID NOS: 982
NUMBER OF SEQ ID NOS: 982
SOFTWARE: FASTSEQ for Windows Version 3.0

; TYPE: PRT ; ORGANISM: Homo sapiens US-09-822-827-944

Query Match Best Local Similarity

98.2%; 98.0%;

Length 750;

SEQ ID NO 944 LENGTH: 750

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Pred. No. 7.3e-217;
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CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/065311
PRIOR APPLICATION NUMBER: 60/065364
PRIOR FILING DATE: 1997-11-21
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APPLICANT: Baker Kevin P
APPLICANT: Botstein, Dav
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Hillan, Kenneth J
Kljavin, Ivar J.
Kuo, Sophia S.
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                       Tumas, Daniel
Williams, P. Mickey
Wood, William I.
                                                       Roy, Margaret Ann
Shelton, David L.
Stewart, Timothy A.
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Gerritsen, Mary E.
Goddard, Audrey
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Botstein, David
                                                                                           Paoni, Nicholas F
                                                                                                         Pan, James;
                                                                                                                   Napier, Mary A.
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Grimaldi, J. Christopher
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Pred. No. 7
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CURRENT APPLICATION NUMBER: US/09/978,697
CURRENT FILING DATE: 2001-10-16 PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR OR FILING DATE: 1998-04-01
OR APPLICATION NUMBER: 60/080333
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OR APPLICATION NUMBER: 60/081070
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OR FILING DATE: 2001-07-30
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PRIOR APPLICATION NUMBER: 60/081195
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         APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Feirara, Napoleon
APPLICANT: Filvaroff, Ellen
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APPLICATION NUMBER: 60/085580
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APPLICATION NUMBER: 60/085573
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        Eaton, Dan
Ferrara, Napoleon
Filvaroff, Ellen
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Sherman
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APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630P1C9
CURRENT APPLICATION NUMBER: US/09/978,192A
CURRENT FILING DATE: 2001-10-15
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Shelton, David L.
Stewart, Timothy A.
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Grimaldi, J. Christopher
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Hillan, Kenneth J
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FILING DATE: 1998-04-15
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APPLICATION NUMBER: 60/081838
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FILING DATE: 1998-04-09
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PRIOR APPLICATION UNMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
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TITLE OF INVENTION: Acids Encoding the
FILE REFERENCE: P2630P1663
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Williams, P. Mickey
Wood, William I.
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Hillan, Kenneth J
Kljavin, Ivar J.
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Grimaldi, J. C
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Baker Kevin P.
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Pred. No. 7.3e-217;
6; Mismatches 3;
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; SOFTWARE: FASTSEQ 1
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; LENGTH: 750
; TYPE: PRT
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER FILE REFERENCE: 210121.534C2
CURRENT APPLICATION NUMBER: US/09/895,793
CURRENT FILING DATE: 2001-06-29
NUMBER OF SEQ ID NOS: 982
SOFTWARE: FastSEQ for Windows Version 3.0
Query Match
Best Local Similarity
Matches 433; Conserv
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Mitcham, Jennifer L.
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Vinals de Bassols, Carlota
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Vedvick, Thomas S
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Hepler, William
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same FILE REFERROCE: PESG30P1C7
CURRENT APPLICATION NUMBER: US/09/978,189
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: 09/918585
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
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Grimaldi, J. Christopher
Gurney, Austin L.
Hillan, Kenneth J
Kljavin, Ivar J.
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Baker Kevin P.
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                                                                                                                    Tumas, Daniel Williams, P. Mickey Wood, William I.
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Shelton, David L.
Stewart, Timothy A.
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Botstein, David
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Napier, Mary A.
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Goddard, Audrey
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J. Christopher
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Pred. No. 7.3e
6; Mismatches
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APPLICATION NUMBER: 60/083496 FILING DATE: 1998-04-29 APPLICATION NUMBER: 60/083499

APPLICATION NUMBER: 60/083554 FILING DATE: 1998-04-29

APPLICATION NUMBER: FILING DATE: 1998-04 FILING DATE: 1998-04-29

1998-04-29

60/083545

APPLICATION NUMBER: 60/083558 FILING DATE: 1998-04-29

APPLICATION NUMBER:

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APPLICATION NUMBER:

FILING DATE:

1998-04-29

60/083500 60/083559

APPLICATION NUMBER: 60/083742 FILING DATE: 1998-04-30

APPLICATION NUMBER: 60/084366

APPLICATION NUMBER: 60/083322 FILING DATE: 1998-04-28 APPLICATION NUMBER: 60/083392

FILING DATE: 1998-04 APPLICATION NUMBER:

FILING DATE:

1998-04-29 1998-04-29

60/083495

APPLICATION NUMBER: 60/082796
FILING DATE: 1998-04-23
APPLICATION NUMBER: 60/083336
FILING DATE: 1998-04-27

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FILING DATE: 1998-05-05 APPLICATION NUMBER: 60/ FILING DATE: 1998-05-06

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APPLICATION NUMBER: 60/084441

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FILING DATE: 1998-05-07
APPLICATION NUMBER: 60/084640

NUMBER: 60/084598: 1998-05-07

60/084639

APPLICATION NUMBER: 60/084637 FILING DATE: 1998-05-07

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APPLICATION NUMBER: 60/084643 FILING DATE: 1998-05-07

APPLICATION NUMBER: 60/085339 FILING DATE: 1998-05-13 APPLICATION NUMBER: 60/ FILING DATE: 1998-05-13

60/085338

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RESULT 9
US-09-978-585A-618
Sequence 618, Application US/09978585A
Publication No. US20030049633A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Botstein, David
APPLICANT: Botsoyers, Luc
APPLICANT: Eaton, Dan
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LENGTH: 750
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Best Local
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APPLICANT:
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Hillan, Kenneth
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Kuo, Sophia S.
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Pred. No. 7.3e-217;
6; Mismatches 3;
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SEQ ID NO 618
LENGTH: 750
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CURRENT APPLICATION NUMBER: US/09/978,585A
CURRENT FILING DATE: 2001-10-16
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                        KRQISVAAFTVQAAAETLSEVA 442
                                                                MFLERAFIDPLGLPDRPFYRHVIYAPSSHNKYAGESFPGIYDALFDIESKVDPSKAWGDV
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                                                                                                                 DKIYNISMKHPQEMKTYSLSFDSLFSAVKNFTEIASKFSERLQDFDKSNPILLRMMNDQL
 KRQIYVAAFTVQAAAETLSEVA
                                                 MFLERAFIDPLGLPDRPFYRHVIYAPSSHNKYAGESFPGIYDALFDIESKVDPSKAWGEV
                                                                                                     DKIYSISMKHPQEMKTYSVSFDSLFSAVKNFTEIASKFSERLQDFDKSNPIVLRMMNDQL 668
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Hillan, Kenneth J
Kljavin, Ivar J.
Kuo, Sophia S.
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Godowski, Paul J.
Grimaldi, J. Christopher
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Stewart, Timothy A.
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CURRENT APPLICATION NUMBER: US/09/978,191A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT FILING DATE:
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APPLICANT: Wood, William I.
APPLICANT: Wood, William I.
APPLICANT: Wood, William I.
BITLE OF INVENTION: Acids Encoding the Same
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APPLICANT: Baker Kevin P
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                                                                                  APPLICATION NUMBER: 60/078939
FILING DATE: 1998-03-20
APPLICATION NUMBER: 60/079294
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                                  APPLICATION NUMBER: 60/0
FILING DATE: 1998-03-26
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FILING DATE: 1998-03-12
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FILING DATE: 1997-11-21
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                   APPLICATION NUMBER:
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Shelton, David L.
Stewart, Timothy A.
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Hillan, Kenneth J
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Grimaldi, J. Christopher
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Gerritsen, Mary E.
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Botstein, David
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                                                                                                                                                                                                                                           NUMBER: 60/078004
1998-03-13
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NUMBER: 60/079664
1998-03-27
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PRIOR PRIOR PRIOR PRIOR OR APPLICATION NUMBER: 60/081819
OR FILING DATE: 1998-04-15
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R APPLICATION NUMBER: 60/07
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APPLICATION NUMBER: 60/081817
THE DATE: 1998-04-15 APPLICATION NUMBER: 60/083392 FILING DATE: 1998-04-29 APPLICATION NUMBER: 60/083495 FILING DATE: 1998-04-29 APPLICATION NUMBER: 60/ FILING DATE: 1998-04-27 APPLICATION NUMBER: 60/ FILING DATE: 1998-04-28 FILING DATE: 1998-04-22
APPLICATION NUMBER: 60/082797
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DR FILLING DATE: 1998-05-07
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FILING DATE: 1998-05-07
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FILING DATE: 1998-05-13
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APPLICATION NUMBER: 60/084598
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APPLICATION NUMBER: 60/083742
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                                                 LGSTEWAEDNSRLLQERGVAYINADSSIEGNYTLRVDCTPLMYSLVYNLTKELKSPDEGF
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Pred. No. 7.3e-217;
6; Mismatches 3;
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APPLICANT: WILLIAMS, F. MICKEY
APPLICANT: WOOD, WILLIAM I.

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucl
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630F1C17

CURRENT APPLICATION NUMBER: US/09/978,403A

CURRENT FILING DATE: 2002-03-19

PRIOR APPLICATION NUMBER: 09/918585

PRIOR FILING DATE: 2001-07-30

PRIOR FILING DATE: 1997-10-17

PRIOR APPLICATION NUMBER: 60/062250

PRIOR FILING DATE: 1997-11-03

PRIOR APPLICATION NUMBER: 60/064249

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PRIOR APPLICATION NUMBER: 60/064249

PRIOR FILING DATE: 1997-11-13

PRIOR APPLICATION NUMBER: 60/065311

PRIOR FILING DATE: 1997-11-13

PRIOR APPLICATION NUMBER: 60/065364

PRIOR APPLICATION NUMBER: 60/077450

PRIOR FILING DATE: 1997-11-21

PRIOR PRIOR DATE: 1998-03-10

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APPLICATION FILING DATE:
                                    FILING DATE: 1998-03-11
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Grimaldi, J. Christopher
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Filvaroff,
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Kuo, Sophia S.
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Desnoyers, Luc
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                  NUMBER:
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APPLICATION NUMBER: 60/077649
FILING DATE: 1998-03-11
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FILING DATE: 1998-03-12
APPLICATION NUMBER: 60/077791

APPLICATION NUMBER: 60/078004 FILING DATE: 1998-03-13

																																																								
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PRIOR APPLICATION NUMBER: 60/080105

PRIOR APPLICATION NUMBER: 60/080105

PRIOR APPLICATION NUMBER: 60/080107

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PRIOR APPLICATION NUMBER: 60/08194
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Roy, Margaret Ann
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          Tumas, Da
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Kuo, Sophia S.
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Hillan, Kenneth
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Gerritsen, Mary E.
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CURRENT APPLICATION NUMBER: US/09/978,564A CURRENT FILING DATE: 2001-10-16 PRIOR APPLICATION NUMBER: US/09/978,564A
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RESULT 13
US-09-999-833A-618
Sequence 618, Application US/09999833A
Publication No. US20030054405A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
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PRIOR APPLICATION NUMBER: 60/085339
PRIOR FILING DATE: 1998-05-13
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PRIOR APPLICATION NUMBER: 60/085323
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085582
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PRIOR APPLICATION NUMBER: 60/08569
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PRIOR APPLICATION NUMBER: 60/08579
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APPLICATION NUMBER: FILING DATE: 1998-0

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DR APPLICATION NUMBER: 60/083500
R FILING DATE: 1998-04-29
DR APPLICATION NUMBER: 60/083742
DR FILING DATE: 1998-04-30
DR APPLICATION NUMBER: 60/084366
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APPLICATE: 1998-05-06

APPLICATION NUMBER: 60/084637 FILING DATE: 1998-05-07

PR APPLICATION NUMBER: 60/084639
PR FILING DATE: 1998-05-07
PR APPLICATION NUMBER: 60/084640
PR FILING DATE: 1998-05-07
PR APPLICATION NUMBER: 60/084598
PR FILING DATE: 1998-05-07
PR APPLICATION NUMBER: 60/084600

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1998-05-07

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APPLICATION NUMBER: 60/083558
FILING DATE: 1998-04-29

DR APPLICATION NUMBER: 60/083495

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RR FILLING DATE: 1998-04-29

DR APPLICATION NUMBER: 60/083499

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DR APPLICATION NUMBER: 60/083545

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DR APPLICATION NUMBER: 60/083554

APPLICATION NUMBER: 60/083322 FILING DATE: 1998-04-28 APPLICATION NUMBER: 60/083392 FILING DATE: 1998-04-29

APPLICATION NUMBER: 60/083336 FILING DATE: 1998-04-27

OR APPLICATION NUMBER: 60/082700
OR FILLING DATE: 1998-04-22
OR APPLICATION NUMBER: 60/082797
OR FILLING DATE: 1998-04-22
OR APPLICATION NUMBER: 60/082796
OR FILING DATE: 1998-04-23

APPLICATION NUMBER: 60/ FILING DATE: 1998-04-22

60/082804

APPLICATION NUMBER: 60/082569 FILING DATE: 1998-04-21 APPLICATION NUMBER: 60/082704 FILING DATE: 1998-04-22

FILING DATE: 1998-04-15 APPLICATION NUMBER: 60/082568 FILING DATE: 1998-04-21

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APPLICATION NUMBER: 60/081819
FILING DATE: 1998-04-15

APPLICATION NUMBER: 60/081229 FILING DATE: 1998-04-09

APPLICATION NUMBER: 60/081203 FILING DATE: 1998-04-09

APPLICATION NUMBER: FILING DATE: 1998-0 APPLICATION NUMBER:

NUMBER: 60/ : 1998-04-08 1998-04-08

60/081195 60/081071

APPLICATION NUMBER: 60 FILING DATE: 1998-04-1

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CURRENT FILING DATE: 2001-10-24
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/065311
PRIOR APPLICATION NUMBER: 60/066364
PRIOR FILING DATE: 1997-11-21
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CURRENT APPLICATION NUMBER: US/09/999,833A
CURRENT FILING DATE: 2001-10-24
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OR FILING DATE: 1998-03-10
OR APPLICATION NUMBER: 60/077632
OR FILING DATE: 1998-03-11
OR APPLICATION NUMBER: 60/077641
OR APPLICATION NUMBER: 60/077649
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Williams, P. Mickey
Wood, William I.
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Shelton, David L.
Stewart, Timothy A.
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Grimaldi, J. Christopher
Gurney, Austin L.
Gurney, Kenneth J
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OR FILING DATE: 1998-05-07
OR APPLICATION NUMBER: 60/084643
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OR FILING DATE: 1998-05-07
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FILING DATE: 1998-05-13
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APPLICATION NUMBER:
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FILING DATE: 1998-05-05
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FILING DATE: 1998-05-06
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                                                                                              DRYVILGGHRDSWVFGGIDPQSGAAVVHETVRSFGTLKKEGWRPRRTILFASWDAEEFGL
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RESULT 14
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CURRENT FILING DATE: 2001-10-16
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR PPLICATION NUMBER: 60/062250
PRIOR PPLICATION NUMBER: 60/062249
PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/064249
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APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630P1C12
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APPLICANT: Baker Kev
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OR APPLICATION NUMBER: 60/066364
OR FILING DATE: 1997-11-21
OR FILING DATE: 1997-21-21
OR APPLICATION NUMBER: 60/077450
OR FILING DATE: 1998-03-10
OR APPLICATION NUMBER: 60/077632
OR FILING DATE: 1998-03-11
OR APPLICATION NUMBER: 60/077641
OR APPLICATION NUMBER: 60/077649
OR FILING DATE: 1998-03-11
OR APPLICATION NUMBER: 60/077791
OR APPLICATION NUMBER: 60/07791
OR FILING DATE: 1998-03-12
OR APPLICATION NUMBER: 60/078004
OR FILING DATE: 1998-03-12
OR APPLICATION NUMBER: 60/078004
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OR APPLICATION NUMBER: 60/078066
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Baker Kevin P.
Botstein, David
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Shelton, David L.
Stewart, Timothy A.
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Gerritsen, Mary E.
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Hillan, Kenneth J
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o. US20030054986A1
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Sophia S.
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f, Ellen
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NUMBER: 60/0: 1998-03-20

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FILING DATE: 1998-03-30 APPLICATION NUMBER: 60/079923

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1998-03-31 1998-03-30

60/080105

APPLICATION N FILING DATE:

NUMBER: 60/080165: 1998-03-31

998-03-31

60/080107

PRIOR

APPLICATION NUMBER: FILING DATE: 1998-03 APPLICATION NUMBER:

.998-03-27

60/079786

60/079920

PRIOR

FILING DATE: 1998-03-27
APPLICATION NUMBER: 60/079663
FILING DATE: 1998-03-27
APPLICATION NUMBER: 60/079728
FILING DATE: 1998-03-27

FILING DATE: 1998-03-26
APPLICATION NUMBER: 60/079664
FILING DATE: 1998-03-27
APPLICATION NUMBER: 60/079689

NUMBER: 60/079656 NUMBER: 60/079294

1998-03-

DATE: 1998-04-23

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APPLICATION NUMBER: 60/081070 FILING DATE: 1998-04-08 APPLICATION NUMBER: 60/081049

APPLICATION NUMBER: 60/080333 FILING DATE: 1998-04-01 APPLICATION NUMBER: 60/080334

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PRIOR APPLICATION NUMBER: 09/918585 PRIOR FILING DATE: 2001-07-30 PRIOR APPLICATION NUMBER: 60/062250 PRIOR FILING DATE: 1997-L0-17 PRIOR APPLICATION NUMBER: 60/064249
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Shelton, David L.
Stewart, Timothy A.
Tumas, Daniel
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Hillan, Kenneth J
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Grimaldi, J. Christopher
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APPLICATION NUMBER: 60/080327
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APPLICATION NUMBER: 60/078939
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APPLICATION NUMBER: 60/066364
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APPLICATION NUMBER: 60/080194
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APPLICATION NUMBER: 60/
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RAPPLICATION NUMBER: 60/084414

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PR APPLICATION NUMBER: 60/083496

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DR FILING DATE: 1998-04-23
R FILING DATE: 1998-05-07
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/cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/B_COMB.pep:*
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PCT-US95-11720-18
US-08-325-553-2
US-08-394-152A-2
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US-08-08-477E-101
US-08-547-197-1
US-08-547-197-2
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US-09-091-889A-2
US-09-634-238-271
US-08-305-477E-11
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US-08-528-122-18
     Query Match
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91	91	91.5	93.5	93.5	93.5	94	94.5	94.5	94.5	95.5	95.5	96	96	96.5	96.5	96.5	96.5
3.9	3.9	3.9	4.0	4.0	4.0	4.0	4.1	4.1	4.1	4.1	4.1	4.1	4.1	4.1	4.1	4.1	4.1
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Sequence 2, Appli	Sequence 2, Appli	Sequence 3242, Ap	Sequence 1, Appli	2	Sequence 1, Appli	Sequence 4067, Ap	Sequence 5007, Ap	Sequence 5179, Ap	Sequence 3229, Ap	Sequence 2, Appli	Sequence 32073, A	Sequence 2, Appli	Sequence 2, Appli	2	•		Sequence 2, Appli

ALIGNMENTS

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Sequence 18, Application US/08528122 Patent No. 5726044
                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-248-7000
TELEPAX: 617-248-7100
INFORMATION FOR SEQ ID NO: 18:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: LO, KIN-MING
APPLICANT: SUDO, YUKIO
APPLICANT: GILLIES, STEPHEN D.
TITLE OF INVENTION: EXPRESSION AND EXPORT TECHNOLOGY (
TITLE OF INVENTION: PROTEINS AS IMMUNOFUSINS
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: PATENT ADMINISTRATOR, TESTA, HURWITZ &
ADDRESSEE: THIBEAULT
ADDRESSEE: THIBEAULT
                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 707 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/528,122
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: PITCHER, EDMUND R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
NAME/KEY: Protein LOCATION: 1..707 OTHER INFORMATION: OTHER INFORMATION:
                                                                                                          MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: MA
COUNTRY: US
ZIP: 02110
                                                                                                                               STRANDEDNESS: single TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                               NAME: PITCHER, EDMUND R. REGISTRATION NUMBER: 27,
                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER: 27,829
REFERENCE/DOCKET NUMBER: FI
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Length 707;

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Matches
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                                     TELEFAX: 617-248-7100 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                              REGISTRATION UMBER: 27,829
REFERENCE/DOCKET NUMBER: FI
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-248-7000
                                                                                                                                        CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: PITCHER, EDMUND R.
                                                                                                                                                                                                          SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: EXTITLE OF INVENTION: PRINTED OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                              STATE: MA
COUNTRY: US
ZIP: 02110
                                                                                                                                                                                 APPLICATION NUMBER: FILING DATE:
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                        LENGTH:
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                                                                                                                  /AGENT INFO...
PITCHER, EDMUND R.
PITCHER, 27,829
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                                                                                                                                                                                                                                                                                                                       Sequence 2,
Patent No. 5
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                                                                                                                                                                                                                                                                                             GENERAL INFORMATION: APPLICANT: Israel
                                                                                                                                                                                                                                     APPLICANT: Heston, WE APPLICANT: Fair, Will TITLE OF INVENTION: TOUR NUMBER OF SEQUENCES:
                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
COMPUTER: IBM PC com
                                       CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: FEATURE:
                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY:
LOCATION:
                                                                                                                                                                 STREET: 30 Rock
CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION:
                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CLASSIFICATION:
                           FILING DATE:
                                                                                                                                          ZIP: 10112
                                                                                                                                                  COUNTRY:
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                                                                                                                                                                                                                                                                                                                       , Application 5538866
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Pred. No. 1.6e-214;
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                                                                                                                                                                          Sequence 2, Application US/08394152A Patent No. 5935818 GENERAL INFORMATION:
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Best Local :
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TELEX: 422523 COOP UI
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
TEN amino acids
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ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 1747/41426
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 977-9550
TELEPHONE: (212) 664-0525
                                                                          APPLICANT: Israeli, Ron S.
APPLICANT: Heston, Warren D.W.
APPLICANT: Fair, William R.
TITLE OF INVENTION: PROSTATE-SPECI
TITLE OF INVENTION: USES THEREOF
NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
        STREET: NE STATE: NE COUNTRY:
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amino acid
OGY: linear
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Similarity 98.0%;
33; Conservative
                                   r: 1185 Avenue of the New York
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Pred. No. 1.8e-214;
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Best Local Similarity
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TELEPAX: (212) 391-0525
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 750 amino acids
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NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 41.
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein
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                                                           KRQIYVAAFTVQAAAETLSEVA 750
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Pred. No. 1.8e-214;
6; Mismatches 3;
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GENERAL INFORMATION:
APPLICANT: Murphy, Gerald P.
APPLICANT: Boynton, Alton L.
APPLICANT: Holmes, Eric H.
APPLICANT: Tino, William Thomas
APPLICANT: Tino, William Thomas
TITLE OF INVENTION: MONOCLONAL ANTITILE OF INVENTION: FOR THE EXTRAC

MONOCLONAL ANTIBODIES SPECIFIC FOR THE EXTRACELLULAR DOMAIN OF PROSTATE-SPECIFIC

MEMBRANE ANTIGEN

Sequence 2, Patent No.

2, Application o. 6150508

US/09044668

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Best Local S
Matches 433
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APPLICATION NUMBER:
FILING DATE:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Baldwin, Geraldine F
REGISTRATION NUMBER: 31,232
REFERENCE/DOCKET NUMBER: 8511
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
TELEFAX: 650-493-556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIIM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie &
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CITY: Ne
STATE: N
COUNTRY:
COUNTRY:
2IP: 100
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TOPOLOGY: lir
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1155 Avenue of the Americas
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llarity 98.0%;
Conservative
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CURRENT APPLICATION NUMBER: US/08/705,477E
CURRENT FILING DATE: 1996-08-29
NUMBER OF SEQ ID NOS: 128
SOFTWARE: Patentin version 3.1
SEQ ID NO 2
LENGTH: 750
TYPE: PRT
ORGANISM: Homo sapiens
US-08-705-477E-2
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US-08-705-477E-2
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                                                                                                                     Sequence 101, Application Patent No. 6569432 GENERAL INFORMATION:
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APPLICANY: Israell, Ron S
APPLICANY: Heston, Warren D.W.
APPLICANT: Fair, William R.
APPLICANT: Overfelli, Ouathek
APPLICANT: Pinto, John
TITLE OF INVENTION: PROSTATE-SPECIFIC MEMBRANE.
FILE REFERENCE: 1769/41426-G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2, Applic Patent No. 6569432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 433;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local
APPLICANT: Pinto, John TITLE OF INVENTION: PROSTATE-SPECIFIC MEMBRANE FILE REFERENCE: 1769,441426-G CURRENT APPLICATION NUMBER: US/08/705,477E
                                                          APPLICANT: APPLICANT:
                                                                                       APPLICANT: Israeli, APPLICANT: Heston,
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                                                          Fair, William
Overfelli, Oua
                                                                                       Heston, Warren
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98.0%;
                                                           Ouathek
                                                                                                                                                   US/08705477E
                                                                                         D.W.
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Pred. No. 1.8e-214;
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; SOFTWARE: PatentIn versic
; SEQ ID NO 101
; LENGTH: 693
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-08-705-477E-101
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Best Local Similarity
                                                                                                                           COUNING
ZIP: 14603
COMPUTER READABLE FORM:
COMPUTER: ELOPPY disk
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: FORM:
MEDIUM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                            OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Gong, Joseph K.

APPLICANT: Glomski, Chester A.

TITLE OF INVENTION: A METHOD FOR DETECTING A MAMMAL'S PRIOR

TITLE OF INVENTION: EXPOSURE TO RADIATION OR RADIOMIMETIC AGENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
ATTORNEY/AGENT INFORMATION
                                                                                                                                                                                                                                                                                                                                                STREET: Clinton
CITY: Rochester
STATE: New York
                              CLASSIFICATION:
                                                         FILING DATE:
                                                                                 APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE:
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5. 5691157
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YPLYHSVYETYELVEGFYDPMFKYHLTVAQVRGGMVFELANSIVLPFDCRDYAVVLRKYA
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Clinton Square, P.O
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97.78;
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                                                                                                                                                                                                                                                                                                                                                                                                      Devans & Doyle LLP
. Box 1051
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RESULT 9
US-08-957-940-1
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Best Local S
Matches 118
                                                                                    pequence 1, Application US/08957940
Patent No. 6132981
                                                                           GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 19
TELECOMMUNICATION INFORMATION:
TELEPHONE: (716) 263-1634
             APPLICANT: Gong, Joseph K.
APPLICANT: Glomski, Chester A.
TITLE OF INVENTION: A METHOD F
TITLE OF INVENTION: EXPOSURE T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE:
NUMBER OF SEQUENCES:
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nes 118; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Rogalskyj, Peter REGISTRATION NUMBER: 3
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                                                                                                                                                                                          -----RNQLALATWTIQGVANALS
                                                                                                                                                                                                                        DIESKVDPSKAWGDVKRQISVAAFTVQAAAETLS 439
                                                                                                                                                                                                                                                       REINDRIMKVEYHFLSPYVSPRESPFRHIFWGSGSHTLSALVENLRLRQKNITAFNETLF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                P---IDGKYLYRNSNWISK-----IEELSLDNAAFPFLAYSGIPAVSFCFCED-
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             FOR DETECTING
                OR RADIOMIMETIC
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ZIP: 14603
ZIP: 14603
COMPUTER READABLE FORM:
COMPUTER FIOPPY disk
MEDIUM TYPE: IBM PC compatible
TOMPUTER: THE PC-DOS/MS-DOS

STATE: New York COUNTRY: U.S.A. STREET: Clinton CITY: Rochester CORRESPONDENCE ADDRESS:

ADDRESSEE:

Clinton

Nixon, Hargrave, Devans & Doyle LLP inton Square, P.O. Box 1051

Clinton

Square,

P.O.

Box 1051

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RESULT 10
US-08-547-197-2
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                                                                                                           Sequence 2, Application US/08547197 Patent No. 5691157 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (716) 263-1634
TELEFAX: (716) 263-1600
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 622 amino acids
                                             APPLICANT: Gong, Joseph K.
APPLICANT: Glomski, Chester A.
TITLE OF INVENTION: A METHOD FO
TITLE OF INVENTION: EXPOSURE TO
                 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: 1: MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION: NAME: Rogalskyj, Peter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE:
                                  NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REGISTRATION NUMBER: 38, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER:
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Nixon, Hargrave,
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26.0%;
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Pred. No. 1.2e-34;
9; Mismatches 180
                                             FOR DETECTING A MAMMAL'S PRIOR TO RADIATION OR RADIOMIMETIC AV
 Devans
 & Doyle
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RESULT 11
US-08-957-940-2
; Sequence 2, Application US/08957940
; Patent No. 6132981
; GENERAL INFORMATION:
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (716) 263-1600 INFORMATION FOR SEQ ID NO:
                 APPLICANT: Gong, Joseph K.
APPLICANT: Glomski, Chester A.
TITLE OF INVENTION: A METHOD FI
TITLE OF INVENTION: EXPOSURE TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0.
   NUMBER OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS: single
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REGISTRATION NUMBER: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                       705
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         370 SKNVKLTVSNVLKEIKILNIFGVIKGFVEPDHYVVVGAQRDAWGPGAAKSGVGTALLLKL
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New York
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                                                                                                                                                                                                                                                     SSHNKYAGESFPGIYDALFDIESKVDPSKAWGDV--KRQISVAAFTVQAAAETLS 439
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   SEQUENCES:
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26.5%;
A METHOD FOR DETECTING A MAMMAL'S PRIOR EXPOSURE TO RADIATION OR RADIOMIMETIC AC
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Pred. No. 1.6e-32;
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                  AGENTS
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RESULT 12
US-09-079-955-2
Sequence 2, Application US/09079955A
Patent No. 6465209
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
TELEPHONE: (716) 263-1634
TELEPAX: (716) 263-1600
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/957,940
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Rogalskyj, Peter
REGISTRATION NUMBER: 38,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                    645
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                                                                                                            GSH-----TLPAL---LENLKLRKQNNGAFNETLFRNQLALATWTIQGAANALS 750
                                                                                                                                                                                ARGDFFRATSRLTTDFGNAEKTDRFVMKKLNDRVMRVEYHFLSPYVSPKESPFRHVFWGS
                                                                                                                                                                                                                  AVKNFTEIASKFSERLQDFDKSNPILLRMMNDQLMFLERAFIDPLGLPDRPFYRHVIYAP
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                                                                                                                                                                                                                                                                                    TVAQVRGGMVFELANSIVLPEDCRDYAVVLRKYADKIYNISMKHPQEMKTYSLSEDSLES
                                                                                                                                                                                                                                                                                                                           TLDNAAFPFLAYSGIPAVSFCFCED-----TDYPYLGTTMDTYKELIERIPE-LNKVAR
                                                                                                                                                                                                                                                                                                                                                            GSGNDFEVFFQRLGIASGRARYTKNWETNKFSGYPLYHSVYETY-ELVEKFYDPMFKYHL 266
                                                                                                                                                                                                                                                                                                                                                                                               GTSNFKVSASPLLYTLIEKTMQNVKHP---VTGQFLYQDSNWASK------VEKL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VRSFGTL-KKEGWRPRRTILFASWDAEEFGLLGSTEWAEDNSRLLQERGVAYINADSSIE 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SKNVKLTVSNVLKEIKILNIFGVIKGFVEPDHYVVVGAQRDAWGPGAAKSGVGTALLLKL 429
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            760 amino acids
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26.5%; Pred. No. 1.6e-32;
+1vo 93; Mismatches 172; Indels
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GENERAL INFORMATION:

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APPLICANT: Hene V. Kofod

APPLICANT: Mikio Fujii

APPLICANT: Chigusa Shizuoka

TITLE OF INVENTION: Methods For Producing Protein

TITLE OF INVENTION: Hydrolysates

FILE REFERENCE: 5253,500-0US

CURRENT APPLICATION NUMBER: US/09/079,955A

CURRENT FILING DATE: 1998-05-15

NUMBER OF SEQ ID NOS: 11

SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                       ; ORGANISM: Aspergillus US-09-330-095-1
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US-09-330-095-1
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                                                                                                                                       Query Match
Best Local
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SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1, Application US/09330095
Patent No. 6127161
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LENGTH: 496
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Best Local Similarity
Matches 51; Conserv
                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/330,095
CURRENT FILING DATE: 1999-66-11
EARLIER APPLICATION NUMBER: JP-164611/1998
EARLIER FILING DATE: 1998-06-12
NUMBER OF SEQ ID NOS: 14
                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Kikkoman Corporation TITLE OF INVENTION: Leucine Aminopeptidase Gene, Recombinant DNA, TITLE OF INVENTION: Process for Producing Leucine Aminopeptidase FILE REFERENCE: PH-622
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Elizabeth Golightly APPLICANT: Tony Byun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Alexander Blinkovsky APPLICANT: Kimberly Brown
                                                                                                                                                                                                                     TYPE: PRT
                                                                                                                                                                                                                                        LENGTH: 481
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                                                                                                                       51;
                                                                                                                                       Similarity
VDLWVDSKQENRTTYNVIAQTKGG-DPNNVVALGGHTDSVEAGPGIN-DDGSGIISNLVV
                                                                           VKMHIHSTNEVTRIYNVIGTLRGAVEPDRYVILGGHRDSWVFG-GIDPQSGAAVVHETVR
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                                                                                                                      Conservative
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25.5%;
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25.5%;
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                                                                                                                  Score 131.5; DB 3;
Pred. No. 0.00036;
9; Mismatches 87;
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Pred. No. 0.00024;
9; Mismatches 87
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FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 10292
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US-09-252-991A-18292
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EARLIER FILING DATE: 1998-07-15
EARLIER FILING DATE: 1998-07-15
EARLIER FILING DATE: 1998-07-15
NUMBER: 60/092,956
NUMBER OF SEQ ID NOS: 267
SOFTWARE: PATENTIN VET. 2.0
SEQ ID NO 120
SEQ ID NO 120
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APPLICANT: Rosen et al.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local (
                                                                                                                                                                                                                                         GENERAL INFORMATION: APPLICANT: Marc J.
                                                                                                                                                                                                                                                                          Sequence 18292, Application US/09252991A Patent No. 6551795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
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CURRENT FILING DATE: 2000-01-13
EARLIER APPLICATION NUMBER: E7/US99/15849
EARLIER FILING DATE: 1999-07-14
EARLIER APPLICATION NUMBER: 60/092,921
EARLIER FILING DATE: 1998-07-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: 71 Human Secreted Proteins FILE REFERENCE: PZ030P1
                                                                                                                                                                                             TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: SITE LOCATION: (473)
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ENGTH: 584
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                                                                                                                                                                                                                                                                                                                                                                                                     RPKRTLRLVLWTAEEQGGVGAFQY 346
                                                                                                                                                                                               MARC J. Rubenfield et al.
VENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING
VENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Application US/09482273
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Best Local Similarity
                                                                                                121 LGSTEWAEDNSRLLQERGVAYINADSSIEGNYTLRVDCTPLMYSLVYNLTKELKSPDEGF
                                                                                                                                    339 VMVGAHLDS-VFEGPGINDNGSGSAAQLE----MAVLLAKA-LPVNKVRFAWWGAEEAGL
   439
                               181 EG-----KSLYESWTKKSPSPEFSGMPRISKLGSGNDFEVFFQRLGIASG 225
                                                                                                                                                                                                     284 SYEGGIPVIFATYDNGVAWS---QTPDLQLHLVVDVVRKKTETYNVVAETRRG--NPNNV 338
                                                                                                                                                                   64 VILGGHRDSWVFGG---IDPOSGAAVVHETVRSFGTLKKEGWRPRRTILFASWDAEEFGL
                                                                                                                                                                                                                                   10 SWRGSLKV---SYNVGPGFTGNFSTQKVKMH--IHSTNEVTRIYNVIG-TLRGAVEPDRY 63
                                                                                                                                                                                                                                                                         60;
QGPPGSAAIERLFEAYFRLR-GQQSEG----TEIDFRSDYAEFFNS-GTAFG 484
                                                                    VGSTHYVQNLAPEEKKKIKAYLNFDMIGSPNFG------NFIYDGDGSDFGL
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                                                                                                                                                                                                                                                                                           Score 121.5; DB Pred. No. 0.0047;
                                                                                                                                                                                                                                                                                                           DB 4;
                                                                                                                                                                                                                                                                           84;
                                                                                                                                                                                                                                                                                                           Length 584;
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Search completed: October 4, 2003, 23:26:47
Job time: 37 secs

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Minimum
Maximum
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Perfect score:
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Match
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 283308 seqs, 96168682 residues
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Copyright (c) 1993 - 2003
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T47631
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T40289

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4.4	4.4	4.4	4.4	4.5	4.6	4.6	4.6	4.6	4.6	4.6	4.6	4.8	4.8	4.8	4.9
704	759	855	816	2957	1481	571	449	980	1447	488	411	537	411	411	468
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T01772	JQ1045	A71223	C83424	T33152	S28669	н87600	Н97249	T24556	S63669	A87569	C64783	A54134	E85551	в90701	F87359
hypothetical prote	arylphorin precurs	hypothetical prote	assimilatory nitr	hypothetical prote	pullulanase (EC 3	hypothetical prote	protein containin	hypothetical prote	UDPglucose-glycop	peptidase M20/M25	probable N-carbam	aminopeptidase Y	probable hydantoi	allantoate amidoh	leucine aminopept

A;Cross-references: GB:M99487; NID:g190663; PIDN:AAA60209.1; A;Experimental source: prostatic carcinoma cell line LNCaP A;Note: sequence extracted from NCBI backbone (NCBIN:121724, C;Superfamily: transferrin receptor C;Keywords: surface antigen; transmembrane protein RESULT A56881 Qy C;Accession: A56881
R;Israeli, R.S.; Powell, C.T.; Fair, W.R.; Heston, W.D.
Cancer Res. 53, 227-230, 1993
A;Title: Molecular cloning of a complementary DNA encoding A;Reference number: A56881; MUID:93113576; PMID:8417812
A;Accession: A56881 prostate-specific membrane antigen - human
C;Species: Homo sapiens (man)
C;Date: 03-Nov-1995 #sequence_revision 03-Nov-1995 #text_change В Qy 밁 Qy 밁 δÃ 밁 밁 Q 밁 A; Molecule type: mRNA A; Residues: 1-750 <ISR> A; Status: preliminary Matches Query Match Best Local : 609 301 549 241 489 181 429 121 LGSTEWAEDNSRLLQERGVAYINADSSIEGNYTLRVDCTPLMYSLVYNLIKELKSPDEGF 180 369 309 tch 98.2%; al Similarity 98.0%; 433; Conservative 61 \vdash EGKSLYESWTKKSPSPEFSGMPRISKLGSGNDFEVFFQRLGIASGRARYTKNWETNKFSG DRYVILGGHRDSWVFGGIDPQSGAAVVHETVRSFGTLKKEGWRPRRTILFASWDAEEFGL MGGSAPPDSSWRGSLKVSYNVGPGFTGNFSTQKVKMHIHSTNEVTRIYNVIGTLRGAVEP LGSTEWAEENSRLLQERGVAYINADSSIEGNYTLRVDCTPLMYSLVHNLTKELKSPDEGF DRYVILGGHRDSWVFGGIDPQSGAAVVHEIVRSFGTLKKEGWRPRRTILFASWDAEEFGL MGGSAPPDSSWRGSLKVPYNVGPGFTGNFSTQKVKMHIHSTNEVTRIYNVIGTLRGAVEP EGKSLYESWTKKSPSPEFSGMPRISKLGSGNDFEVFFQRLGIASGRARYTKNWETNKFSG 6, Score 2288; DB 2; Pred. No. 1.8e-163; 6; Mismatches 3; Length Indels þ PID:g190664 NCBIP: 121725) prostate-specific membra 17-Mar-2000 0 Gaps 360 300 488 120 899 548 240 428

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RESULT 3
T47631
Peptidase-like protein - Arabidopsis thaliana
Peptidase-like protein T5N23.80
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
C;Accession: T47631
R;Obermalter, B; Ottenwaelder, B; Duchemin, D; Zeitler, K; Mewes, H.W.; I submitted to the Protein Sequence Database, March 2000
A;Reference number: Z24463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R;Favello, T.; Rifkin, L.; Chiapelli, B. submitted to the EMBL Data Library, February 1997 A;Description: The sequence of C. elegans cosmid A;Reference number: 220745 A;Accession: T30154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 2
T30154
hypothetical protein R57.1 - Caenorhabditis elegans
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A; Introns: 40/1: 145/1; 230/1; 275/3; 313/1; 344/2; 405/1; 453/2; 576/2; 671/2; 713/3
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A; Residues: 1-751 <FAV>
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                                 Duchemin, D.; Zeitler, K.; Mewes, H.W.; Lemcke,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
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                                                                                                                                                                                                                                          A; Status: preliminary; translated
                                                                                                                                                                                                                                                                                                                R;White,
                                                                                                                                                                                                                                                                                                                          Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Genetics:
                                   Query Match
Best Local Similarity
Matches 147; Conserv
                                                                                                                     Map position:
                                                                                                                                                         Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches 141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ns: 326/3; 407/3;
T5N23.80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     678
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     MGGSAPPDSSWRGSLKVSYNVGPGFTGNFSTQKVKMHIHSTNE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24.9%;
                                                 23.4%;
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A; Nolecule type: DNA
A; Molecule type: DNA
A; Mesidues: 1-1483 <WIL>
A; Cross-references: EMBL: Z78417; PIDN: CAB01688.1;
A; Cross-references: Clone C35C5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Accession: T47631
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-703 < OBE>
A;Cross-references: EMBL:AL138650
A;Experimental source: cultivar Columbia;
                                                                                                                                                                                                                                                                                                                                                                                                                                            hypothetical protein C35C5.2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
                                                                                            A; Introns: 61/1; 203/3; 248/1; 293/3; 331/1; 437/1; 485/2; 523/2; 556/1; 595/3; 620/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      463 --VGLTVEETFKSQN-----NIIQRLSRVDS--DFSGFLHHAGIPSIDMYYG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    119 GLLGSTEWAEDNSRLLQERGVAYINADSSIEGNYTLRVDCTPLMYSLVYNLTKELKSPDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  179 GFEGKSLYESWTKKSPSPEFSGMPRISKLGSGNDFEVFFQRLGIASGRARYTKNWETNKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     293 LGGARAP-LEWRNSGRVGPGQRVGPG-----RMVINMTFQGEMKMKKINNVVVTIRGSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MGGSAPPDSSWRGSLKV--SYNVGPGFTGNFSTQKVKMHIHSTNEVTRIYNVIGTLRGAV 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ILLRMMNDQLMFLERAFIDPLGLPDRPFYRHVIYAPSSHNKYAGESFPGIYDALFDIESK 410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YADKIYNISMKHPQEMKTYSLSFDSLFSAVKNFTEIASKFSERLQDF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EADRYVILGNHRDAWTYGAVDPNSGTSALLDISRRFALLLKSGWRPRRTILLCSWDAEEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EPDRYVILGGHRDSWVFGGIDPQSGAAVVHETVRSFGTLKKEGWRPRRTILFASWDAEEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AKRRELNDRLMLYERGFLDAEGIKGKEWFKHLYYGPAAEPESKLGFFPGIADAIAMNASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADYPVYHTAFDSYDWMIHNADPLFHRHVAMAGIWGLLGILLADEPLIPFDYISYADQLQA 565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SGYPLYHSVYETYELVEKFYDPMFKYHLTVAQVRGGMVFELANSIVLPFDCRDYAVVLRK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----SKLLEGKVSVNPLSMAIQEFSLVAKEAADEAKKLKGKSYSKNDVAAA
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                                                                                                                                                                                                                                                                                                                                                                    Library, August 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       93;
  84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 579; DB 2;
Pred. No. 2.2e-35;
                                              Score 545.5;
                    Pred. No. 2.1e-32;
                                                                                                                                                                                                                                                                                               from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        869
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                                              DB 2;
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  181;
                                                                                                                                                                                                                          GSPDB:GN00028; CESP:C35C5
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                                           Length 1483;
  Indels
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  61;
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  Gaps
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RESULT 5
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Mol. Endocrinol. 4, 531-542, 1990
A;Title: Characterization of rat transferrin receptor cDNA:
A;Reference number: A34549; MUID:91125359; PMID:2126342
A;Accession: A34549
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C:Date: 22-Jun-1990 #sequence_revision
C:Accession: A34549
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: mRNA
A; Residues: 1-622 < ROB>
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                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Superfamily: transferrin receptor
                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                           378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             104
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423
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         receptor; transmembrane protein
                                                                                                                                                                                                                                 MGGSAPP----DSSWRGSLKVSYNVGPGFTGNFSTQKVKMHIHSTNEVTRIYNVIGTLRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VIYAPSSHNKYAGESFPGIYDALFDIESKVDPSKAWGDVKRQISVAAFTVQAA 434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGMVFELANSIVLPFDCRDYAVVLRKYADKIYNISMKHPQEM-KTYSL--SFDSLFSAVK 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRRTILFASWDAEEFGLLGSTEWAEDNSRLLQERGVAYINADSSIEGNYTLRVDCTPLMY 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RKIQNIMGYIKGSQEPDKFVLVSNHYDAWTYGAVDPNSGTSTLLEVSRALKQYQNQTGWI 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TRIYNVIGTLRGAVEPDRYVILGGHRDSWVFGGIDPQSGAAVVHETVRSFGTLKKE-GWR 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P---IDGKYLYRNSNWISK----
                                                                                                                                                     GDYGAVGPTEWLEGYLSSLHLKAFTYINLDKVVLGTSNFKVSASPLLYTLMGKIMQDVKH 377
                                                                                                                                                                                                                                                                          AVEPDRYVILGGHRDSWVFGGIDPQSGAAVVHETVRSFG-TLKKEGWRPRRTILFASWDA 115
                                                                                                                                                                                                                                                                                                               MEGNCPPSWNIDSSCK--LELSQN-----QNVKLTVNNVLKETRILNIFGVIKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QFKLLQKTVLELSEIVQRRNVSKLEELPFGSRVDINNRLIEFEKCFINPHGAIGNPQARH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VLFHPSPDNWYDGDAISQVHDLISKISNSTD-SKELGKLSRQLAKEIALVNVA 770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SLVYNLTKELKSPD--EGFEG-KSLYESWTKKSPSPEFSGMPRISKL-GSGNDFEVFFQR 219
                                  ETNKFSGYPLYHSVYETYELVEKFYDPMFKYHLTVAQVRGGMVFELANSIVLPFDCRDYA 293
                                                                                                              PDEGFEGKSLY--ESWTKKSPSPEFSGMPRISKLGSGNDFEVFFQRLGIASGRARYTKNW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NFTEIASKFSERLQDFDKSN------PILLRM-MNDQLMFLERAFIDPLGLPDRPFYRH 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IECILKFTESKILPYDLNEL-----MDDSIFEYLPKLEDRLNKTLMIGTKTDYLLDAQK 658
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NVLRSAAANVEQPNPTEMEQGRKTLYDSWKYYAPSKNNRSTHPYQRIPAGGSDHLPFFDY 554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PARSILFAHWDAEEYGLIGSTEFAEEYRLQLMRRAVAVINMD-LIGGNQTLLGLSNPTVA 494
                                                                                                                                                                                                                                                                                                                                                                                             Conservative
EDYPYLGTKLDTYEILIQKVPQLNQMVRTAAEVAGQFIIKLTHDIELTLDYEMYN
                                                                                                                                                                                                                                                                                                                                                                                                              19.1%;
                                                                                                                                                                                                                                                                                                                                                                                                              Score 445.5; DB 2
Pred. No. 1.9e-25;
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                                                                           IEELSLDNAAFPFLAYSGIPAVSFCFCED-
                                                                                                                                                                                                                                                                                                                                                                                                                                DB 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                  622;
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                                                                                                                                                                                                                                   317
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C;Superfamily: transferrin receptor
C;Keywords: glycoprotein; iron transport; receptor;
F;1-57/Domain: intracellular #status predicted <INT</pre>
                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: GB:M29618; NID:g193272; PIDN:AAA37616.1; C;Comment: This transmembrane glycoprottein exists as a dimer tty acyl groups. The amino end of each chain lies within the embrane, may also serve as an internal signal sequence. C;Comment: The expression of this receptor, involved in the I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Molecule type: protein
A;Residues: 7-19;158-175,'X',177-179;'DESL','AY',189,'IEN',193,'FXEF',195;196,197-208
A;Residues: 7-19;158-175,'X',177-179;'DESL','AY',189,'IEN',193,'FXEF',195;196,197-208
A;Note: these tryptic fragments have been ordered by homology with the human sequence
R;Stearne, P.A.; Pietersz, G.A.; Goding, J.W.
J.Immunol. 134, 3474-3479, 1985
A;Title: cDNA cloning of the murine transferrin receptor: Sequence of trans-membrane
A;Reference number: 149662; MUID:85159078; PMID:2984291
A;Accession: 149662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Species: Mus musculus (house mouse)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change
C;Accession: S29548; A26735; D34550; I49662
R;Trowbridge, I.S.; Domingo, D.L.; Thomas, M.L.; Chain, A.
submitted to the EMBL Data Library, January 1991
A;Reference number: S29548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: protein
A; Residues: 1-82 < ROTE
R; Grego, B.; Van Driel, I.R.; Stearne, P.A.; Goding, J.W.;
Eur. J. Biochem. 148, 485-491, 1985
A; Reference number: A24550; MUID:85203852; PMID:2986964
A; Accession: D24550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A, Title: Endocytosis of the transferrin receptor requires A; Reference number: A26735; MUID:87187639; PMID:3568132 A; Accession: A26735
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                                                                                                                       F;62-89/Domain: transmembrane #status predicted <TMS>F;89-763/Domain: extracellular #status predicted <EXT>F;89-763/Domain: extracellular #status predicted <EXT>F;101-763/Product: 85K serum transferrin receptor #status predicted <MAT>F;253,319,730/Binding site: carbohydrate (Asn) (covalent) #status predict
                                                                                                                                                                                                                                                                                                                                                                                                                   C; Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: mRNA
A; Residues: 'AL', 27-149,'Q', 151-301 <RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: EMBL:X57349; NID:g54914; PIDN:CAA40624.1; PID:g54915 R;Rothenberger, S.; Iacopetta, B.J.; Kuhn, L.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: mRNA
A; Residues: 1-763 <TRO>
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N;Contains: 85K serum transferrin receptor
                                                                                                                                                                                                                                                    F;58-61/Region: stop-transfer sequence
                                                                                                                                                                                                                                                                                                                                                                               A; Description: mediates cell iron uptake by binding, internalizing,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Status: preliminary
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                                 Query Match
Best Local
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                             Local
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                             Similarity
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26.7%;
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Score 435; DB 1; I
Pred. No. 1.5e-24;
88; Mismatches 171;
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                                                              Length 763;
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1 MGGSAPP----DSSWRGSLKVSYNVGPGFTGNFSTQKVKMHIHSTNEVTRIYNVIGTLRG

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J. Biol. Chem. 265, 19077-19081, 1990
A;Title: Serum transferrin receptor is a truncated form of A;Reference number: A36597; MUID:91035436; PMID:2229063 A;Moleonia transferrin receptor is a truncated form of A;Reference number: A36597; MUID:91035436; PMID:2229063 A;Moleonia transferring tra
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Cell 39, 267-274, 1984
A;Title: The human transferrin receptor gene: genomic organization, A;Reference number: A90856; MUID:85048936; PMID:6094009
A;Accession: A90856
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N;Contains: 85K serum transferrin receptor
C;Species: Homo sapiens (man)
C;Date: 25-Feb-1985 #sequence_revision 25-Feb-1985 #text_change 22-Jun-1999
C;Accession: A9334; A90856; A36597; S54327; S09039; A03259
R;Schneider, C; Owen, M.J.; Banville, D.; Williams, J.G.
Nature 311, 675-678, 1984
           R; Alvarez,
Biochem. J.
                                                                                     A; Molecule type: protein
A; Residues: 288-302;694-708;721-730 <COP>
                                                                                                                                                                                                                   A:Experimental source: serum R:Coppolino, M.; Migliorini, M.; Argraves, W.S.; Dedhar, Biochem. J. 306, 129-134, 1995. Biochem. J. 306, 129-134, 1995. Biochem. J. 306 f. 129-134, 1995. Biochem. J. 306 f. 129-134, 1995. Biochem. J. 306, 129-134, 1995. Biochem. J. 306, 129-134, 1995. Biochem. J. 306, 1995. Biochem. J. 306,
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A; Residues: 1-760 <MCC>
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A; Residues: 1-760 <SCH>
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A; Residues: 101-103,'X',105-108,'X',110-119 <SHI>
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R;Shih, Y.J.; Baynes, R.D.; Hudson, B.G.; Flowers, C.H.; Skikne, B.S.; Co
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           transferrin receptor - human
           E.; G
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; Girones, 67, 31-35,
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           N.;
                                                              Davis,
                                                              R.J.
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                                                                                                                                                                                                                                                                                  the alpha(3) integrin PMID:7864799
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A;Description: mediates cell iron uptake by binding, internalizing C;Superfamily: transferrin receptor c;Keywords: glycoprotein; iron transport; receptor; transmembrane F;1-57/Domain: intracellular #status predicted <INT> F;20-24/Region: tyrosine-based endosomal/lysosomal sorting signal F;58-61/Region: stop-transfer sequence F;62-89/Domain: transmembrane #status predicted <TMS> F;62-89/Domain: transmembrane #status predicted <TMS>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: 1-19, 'C', '21-61 <ALV>
A; Residues: 1-19, 'C', '21-61 <ALV>
A; Note: mutant defective in endocytosis
C; Comment: This transmembrane glycoprotein exists as a dimer try acyl groups. The amino end of each chain lies within the embrane, may also serve as an internal signal sequence.
C; Comment: The expression of this receptor, involved in the r
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      F;89-760/Domain: extracellular #status predicted <EXT>F;101-760/Product: 85K serum transferrin receptor #status F;251,317,727/Binding site: carbohydrate (Asn) (covalent)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C; Comment: C; Genetics:
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B
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C; Function:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Cross-references: GDB:120433; OMIM:190010
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                       645 ARGDFFRATSRLTTDFGNAEKTDRFVMKKLNDRVMRVEYHFLSPYVSPKESPFRHVFWGS
                                                                                                                                                                                                                                                                                                                                                                                                                                           490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   370 SKNVKLTVSNVLKEIKILNIFGVIKGFVEPDHYVVVGAQRDAWGPGAAKSGVGTALLLKL 429
                                                                                                                                                                                                                                                                                                                                536 TLDNAAFPFLAYSGIPAVSFCFCED-----TDYPYLGTTMDTYKELIERIPE-LNKVAR 588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               150 GNYTLRVDCTPLMYSLVYNLTKELKSPDEGFEGKSLYE--SWTKKSPSPEFSGMPRISKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            91 VRSFGTL-KKEGWRPRRTILFASWDAEEFGLLGSTEWAEDNSRLLQERGVAYINADSSIE 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                31 TQKVKMHIHSTNEVTRIYNVIGTLRGAVEPDRYVILGGHRDSWVFGGIDPQSGAAVVHET 90 :: ||: : : : | |: | :: | ||: | ||:: :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 110;
                                                   SSHNKYAGESFPGIYDALFDIESKVDPSKAWGDV--KRQISVAAFTVQAAAETLS 439
                                                                                                                                                                                                                                                                         TVAQVRGGMVFELANSIVLPFDCRDYAVVLRKYADKIYNISMKHPQEMKTYSLSFDSLFS
                                                                                                                                                                                                                                                                                                                                                                                    GSGNDFEVFFORLGIASGRARYTKNWETNKFSGYPLYHSVYETY-ELVEKFYDPMFKYHL
                                                                                                                                                                                                                                                                                                                                                                                                                                           GTSNFKVSASPLLYTLIEKTMQNVKHP---VTGQFLYQDSNWASK-----VEKL
GSH-----TLPAL---LENLKLRKQNNGAFNETLFRNQLALATWTIQGAANALS
                                                                                                                                                        AVKNFTEIASKFSERLODFDKSNPILLRMMNDQLMFLERAFIDPLGLPDRPFYRHVIYAP
                                                                                                                                                                                                                  AAAEVAGQFVIKLTHDVELNLDYERYNSQLLSFVRDL----NQYRADIKEMGLSLQWLYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AQMFSDMVLKDGFQPSRSIIFASWSAGDFGSVGATEWLEGYLSSLHLKAFTYINLDKAVL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 426; DB 1;
Pred. No. 7.2e-24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             involved in the regulation
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#status predict
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C;Accession: A48592
R;Collawn, J.F.; Lai, A.; Domingo, D.; Fitch, M.; Hatton, J. Biol. Chem. 268, 21686-21692, 1993
A;Title: YTRF is the conserved internalization signal of A;Reference number: A48592; MUID:94012749; PMID:8408022
A;Accession: A48592
A;Status: preliminary
A;Molecule type: mRNA

transferrin receptor protein - Chinese C;Species: Cricetulus griseus (Chinese C;Date: 03-May-1994 #sequence_revision

hamster) 03-May-1994 hamster

#text_change

20-Aug-1999

Hatton,

the s.;

transferrin receptor,

an

I.S.

A48592

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C;Superfamily: transferrin receptor
C;Keywords: glycoprotein; lipoprotein; phosphoprotein; receptor; thiolester bond; transmers, 19-22/Region: coated pit mediated internalization signal
F;70-88/Domain: transmembrane #status predicted <TRN>
F;23/Binding site: phosphate (Ser) (covalent) #status predicted
F;70/Binding site: palmitate (Cys) (covalent) #status predicted
F;261,326,391,738/Binding site: carbohydrate (Asn) (covalent) #status predicted
                  B
                                          δĀ
                                                                                                                                                                                                                                                                                        A;Cross-references: EMBL:x55348
A;Note: 581-His and 736-Gln were also found as the result of
C;Comment: This protein mediates the endocytosis of the iron
                                                                                                                                                                                                                                                                                                                                                                                              C;Species: Gallus gallus (chicken)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: JH0570; S1685
R;Gerhardt, E.M.; Chan, L.N.L.; Jing, S.; Q1, M.; Trowbridge, I.S.
Gene 102, 249-254, 1991
A;Title: The cDNA sequence and primary structure of the chicken transferrin receptor.
A;Reference number: JH0570; MUID:91340160; PMID:1874449
A;Accession: JH0570
                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: mRNA
A; Residues: 1-776 <GER>
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A;Cross-references: GB:L19142; NID:g304528; PIDN:AAA03576.1; PID:g304529 C;Superfamily: transferrin receptor C;Keywords: endocytosis; glycoprotein; transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    transferrin receptor - chicken
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61
                                                                                                              Similarity
                                          WRG----SLKVSYNVGPGFTGNFSTQKVKMHIHSTNEVTRIYNVIGTLRGAVEPDRYVILG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                WKGAIHSCKVT---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ENLKLRQKNSSAFNETLFRNQLALATWTIQGVANALS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AEKTNRFVVREINNRIMKVEYHFLSPYVSPRESPFRHIFWGSGSHTLTA--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    D-----YDMYNNKILSFYKELNQFRADIKAMGLSLQWLYSARGDFFRATSRLTTDFHN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DCRDYAVVLRKYADKIYNISMKHPQ----EMKTYSLSFDSLFSAVKNFTEIASKFSERLQD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LLGSTEWAEDNSRLLQERGVAYINADSSIEGNYTLRVDCTPLMYSLVYNLTKELKSPDEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DRYIVVGAQRDAWGPGAAKSSVGTGLLLKLAQAFSDMVSRGGFKPSRSIIFASWSAGDFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DRYVILGGHRDSWYFGGIDPQSGAAVVHETVRSFGTL-KKEGWRPRRTILFASWDAEEFG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FDIESKVDPSKAWGDV--KRQISVAAFTVQAAAETLS 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FDKSNPILLRMMNDQLMFLERAFIDPLGLPDRPFYRHVIYAPSSHNKYAGESFPGIYDAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IDGKPLYRDSNWISKVEDLSLDNAAFPFLAYSGIPAVSFWFCENE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEGKSLY--ESWTKK------SPSPEFSGMPRISKLGSGNDFEVFFQRLGIASGRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AVGATEWLEGYLSSLHLKAFTYINLDKVVLGTRNFKVSASPLLYTLIEKTMQDVRHP---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          METNCPP--SWNTDSLCKLESSQGINVNLS-----VNNVLKETRILNIFGVIKGFEEP
                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----DYPYLDTNLDTYEKLIQKVPQLNKMVRAAAEVAGQFIIKLTHDIELNL
                                                                                                        17.8%;
27.1%;
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24.9%; Pred. No. 9.3e-24;
tive 88; Mismatches 182
          -TKHESQIMVKLDVNNSMKDRKILNIFGAIQGFEEPDRYVVIG
                                                                                          84;
                                                                                    Score 413.5; DB 1;
Pred. No. 6.5e-23;
4; Mismatches 175;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        182;
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C; Keywords: transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Cross-references:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
A; Residues: 1-811 <ROS>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Reference number: S56848
A; Accession: S57149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        probable membrane protein YJR126c - yeast (Saccharomyces cerevisiae)
W;Alternate names: hypothetical protein J2050
C;Species: Saccharomyces cerevisiae
C;Date: 23-Aug-1995 #sequence_revision 08-Sep-1995 #text_change 19-A
C;Accession: S57149
R;Rose, M.; Koetter, P.; Entian, K.D.
Submitted to the Protein Sequence Database, September 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 10
S57149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Gene: MIPS:YJR126c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Cross-references: EMBL: Z49626;
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                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
les 119; Conserv
    611
                                            247
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                                                                                                                                                                                                                                                                                                                                          19 YNVGPG-----FTG-NFSTQKVKMHIHSTNEVTRIYNVIGTLRGAVEPDRYVILGGH 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        293
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                                      VYETYELVEKFYDPMFKYHLTVAQVRGGMVFELANSIVLPFDCRDYAVVLRKYADKIY--
                                                                                                              WTKKSPSPEFSGMPRISKLGSGNDFEVFFQRLGIASGRARYTKNWETNKFSGYPLYH--S 246
                                                                                                                                                    AHAAILRRRALVYLNLDNAISGT-NFHCKANPLLQDVIYEAAK--LTEFNGHEDWSLFDH 562
                                                                                                                                                                                DNSRLLQERGVAYINADSSIEGNYTLRVDCTPLMYSLVYNLTKELKSPDEGFEGKSLYES 188
                                                                                                                                                                                                                                                                                                      FQIGPGSNIKDFGSFTGPSSSIDKVHLHNELTYNIKEMSSVEVSIPG-IFTEGEIIIGAH 445
                                                                                                                                                                                                                                RDSLASSSAGDANSGSATLLEIARGMSKLLKHGWKPLRPIKLISWDGERSGLLGSTDYAE
                                                                                                                                                                                                                                                                RDSWVFGGI-DPQSGAAVVHETVRSFGTLKKEGWRPRRTILFASWDAEEFGLLGSTEWAE 128
VFDSPTWLEKFTNSDYKLHNTMAMFVGLTTLMLSENELARFN-----THVYLKKIYNW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DPSKAWGDVKRQISVAAFTVQAAAETL 438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LRMMNDQLMFLERAFIDP-LGLPDRPFYRHVIYAPSSHNKYAGESFPGIYDALFDIESKV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEELLAYQEEF----LPYIKEVRELGLTLDWLFFARGDFQRAVTALRRDIANSDGENRVI 686
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AVVLRKYADKIYNISMKHPQEMKTYSLSFDSLFSAVKNFTEIASKFSERLQDFDKSNPIL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AQRDSWGPGVAKAGTGTAILLELARVISDIVKNEGYKPRRSIIFASWSAGDYGAVGATEW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GHRDSWVFGGIDPQSGAAVVHETVRSFGTL-KKEGWRPRRTILFASWDAEEFGLLGSTEW 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      --- NKDEEYRFLDTKGDTLENLRKI-DNLDALLAAAAEVAGQAALRLTHDHELFLDIGRY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E----SWTK-----KSPSPEFSGMPRISKLGSGNDFEVFFQRLGIASGRARYTKN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LEGYSAMLHAKAFTYISLDAPVLGASHVKISASPLLYMLLGSIMKGVKNP--AAVSESLY
                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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                                                                          -KYTSNATISLLDGLSSYTSFQYHLGVPAAHFQF----NANDTSG-AVYHSNS 610
                                                                                                                                                                                                                                                                                                                                                                                                      17.1%;
27.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NID:g1015854;
                                                                                                                                                                                                                                                                                                                                                                                                        Score 399; DB 2;
Pred. No. 8.4e-22;
                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                      164;
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The Cold

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RESULT 11
T40289
hypothetical protein SPBC354.09c - fission yeast (Schizosaccharomyces pombe)
hypothetical protein SPBC354.09c - fission yeast (Schizosaccharomyces pombe
C:Species: Schizosaccharomyces pombe
C:Species: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar-2000
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C; Accession: T40289
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C; Superfamily: s
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A;Molecule type: DNA
A;Residues: 1-794 <WOO>
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probable peptidase [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 16-Feb-2001
C;Accession: E85075
                                                                               RESULT 12
E85075
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Local Similarity 25.0%;
nes 105; Conservative (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WRGSLKVSYNVGPGFTGNFSTQKVKMHIHSTNEVTRIYNVIGTLRGAVEPDRYVILGGHR 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NSRLLQERGVAYINADSSIEGNYTLRVDCTPLMYSLYYNLTKELKSPDEGFEGKSLYESW 189
                                                                                                                                                                                                                                                                                                                                                                                                DYTS-----TPMPFLGSCED
                                                                                                                                                                                                                                                                                                                                                                                                                                     TKKSPSPEFSGMPRISKLGSGNDFEVFFQRLGIASGRARYTKNWETNKFSGYPLYHSVYE 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WKESLEAKAVAYINVDVAVSGD-TFTARTVPGLKKVIQRAFDVANEEDEMKAANIITDDF
                                                                                                                                                                                                                                                                            HPQEMKTYSLSFDSLFSAVKNFTEIASKFSERLQDFD-----KSNPILLRMMNDQLMFLE
                                                                                                                                                                                                                                                                                                                                                       TYELVEKFYDPMFKYHLTVAQVRGGMVFELANSIVLPFDCRDYAVVLRKYADKIYNISMK 309
                                                                                                                                                                                                                                                                                                                    TVSWIDTFGSEYWENAARLGKIWSYLILFLANDPVVPYDLEDEINGVGEMLKRIPEIPGA 667
                                                                                                                                                                                                                                         NALDLRKINEEFSELLESLIRFEDEIREWKSLMMHNSYTVSVKKHP-ELEGYNAKLARFE
                                                                                                                                                             RSFLDEAGLPGHEWYKHLIYGPNLRNSHS-QLFPSIFDALLYGDVEA-----AQKEVKR
                                                                                                                                                                                              RAFIDPLGLPDRPFYRHVIYAPSSHNKYAGESFPGIYDALF--DIESKVDPSKAWGDVKR 422
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Pred. No. 1.6e-18;
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R;anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Col
Nature 402, 769-777, 1999
A;Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.
A;Reference number: A85001; MUID:20083488; PMID:10617198
A;Accession: E85075
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A;Molecule type: DNA
A;Residues: 1-280 <STO>
A;Cross-references: GB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           probable membrane protein YOR256c - yeast (Saccharomyces cerevisiae)
N;Alternate names: hypothetical protein O5330
C;Species: Saccharomyces cerevisiae
C;Species: Saccharomyces cerevisiae
C;Date: 12-Jul-1996 #sequence_revision 12-Jul-1996 #text_change 19-Apr-2002
C;Date: 12-Jul-1996 #sequence_revision 12-Jul-1996 #text_change 19-Apr-2002
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S67153
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                                                                                                                                                                                                                                                                                                                                                                                                                   A;Map position: 15R
C;Superfamily: secretory protein SSP134
C;Keywords: transmembrane protein
F;126-142/Domain: transmembrane #status predicted <TMM>
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A; Residues: 1-809 <JAU>
A; Cross-references: EMBL: 275164; NID: g1420578; PIDN: CAA99478.1;
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A; Accession: S67153
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A;Cross-references: S
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                                                                                                                                                                                                                                           RTILFASWDAEEFGLLGSTEWAEDNSRLLQER------GVAYINADSSIEGNYTLR 155
                                                                                                                                                                                                                                                                               IPNIVGKIEGREOSDKAIIIAASRNSINFGTTYPNFGTAALLSIVOLFQEVKYKFGWKPL
                                                                                                                                                                                                                                                                                                              IYNVIGTLRGAVEPDRYVILGGHRDSWVFGGIDPQSGAAVVHETVRSFGTLK-KEGWRPR 105
                                  YHLTVAQVRGGMVFELANSIVLPFDCRDYAVVLRKYADKIYNISMKHPQEMKTYSLSFDS
                                                                                                     VFFQRLGIASGRARYTKNWETNKFSGYPLYHSVYETYELVEKFYDP------
                                                                                                                                       IETHPLLKKF-FURNAH-GNFDISVDNVQHYGDWT----PFLANGIP-VSVISSD----
                                                                                                                                                                          VDCTPLMYSLVYNLTKELKSPDEGFEGKSLYESWTKKSPSPEF-SGMPRISKLGSGNDFE 214
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                                                                                                                                                                                                                                                                                                                                                         78; Mismatches
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pred. No. 1.9e-11;
6; Mismatches 27;
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Pred. No. 6.4e-10;
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   -VEDIDERLORLEQAYPEK---
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                                                                           --DKFERVEKILEDEQNQQSVKDLLVYL 629
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A;Cross-references: GB:AE003921; GB:AE003849; NID:g9105710; PIDN:AAF83630.1; GSPDB:GN A;Cross-references: GB:AE003921; GB:AE003849; NID:g9105710; PIDN:AAF83630.1; GSPDB:GN A;Experimental source: strain 9a5c R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R. Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer as-Neto, E.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer submitted to GenBank, June 2000

A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Franco, J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; La chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, A;Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, Rodrigues, V.; Rosa, A.J. de M.; de Rodrigues, V.; Rosa, A.J. de M.; de N.; de Salva, R.G.; Santelli, R.V.; Sanda, A;Authors: da Silva, A.G.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silva, A;Authors: da Silva, A.G.R.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 15-Sep-2000
C;Accession: G82759
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C; Superfamily:
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A; Contents: annotation
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A; Status: preliminary
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A; Residues: 1-529 <SIM>
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Matches
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439
                                                                                                                                                                                                                                                                               330 LARGFA----RGPQPQRSVLFLAVTAEEKGLLGS-EYYASNPLYPLEKTVAVINMDVMNP 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            394 GESFPGIYDALFDIESKVDPSKAW--GDVKRQISVAAF-TVQAAAETLSEV 441
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                                                                     196 PEFSGMPRISKLGSGNDFEVFFQRLGIASGRA 227
                                                                                                                                           385 QGPTRDFGIYGTAKLDLLDMLKQVAAGWKLRYTLD---PTPEAGHFFRSDHFSFAKR---
                                                                                                                                                                                                             146 ---SSIEGNY-TLRVDCTPLM-----YSLVYNLTKELKSPDEGFEGKSLYESWTKKSPS 195
                                                                                                                                                                                                                                                                                                                                                                                                                       270 SEVITSHNVAARLQGCAHPDETVIYSAHWDHLGVGAPDAKGDTIFNGALDNASGTAALLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            42 NEVTRIYNVIGTLRGAVEPDRYVILGGHRD-----SWVF-GGIDPQSGAAVVHE 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  l Similarity
66; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7.4%; Score 173; DB 2; Length 529; llarity 31.1%; Pred. No. 4e-05; Conservative 30; Mismatches 70; Indels
-GIPAIS-YSAGQDMEVG----GVAAGKA 461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----VDKGDPLRSWTFPEIRDTIAIKDWSSVQVQANTLGTI 761
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      46;
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Search completed: October 4, Job time: 41 secs

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                                                                                                                                                                                                                                                                                   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
     2329
2097.5
571.5
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1: sp_archea:*
2: sp_bacteria
3: sp_fungi:*
4: sp_human:*
5: sp_inverteb
6: sp_mammal:*
7: sp_mhc:*
8: sp_organel1
9: sp_phage:*
      100.0
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2329
1 MGGSAPPDSSWRGSLKVSYN......QISVAAFTVQAAAETLSEVA 442
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Gapop 10.0 , Gapext 0.5
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sp_vertebrate:*
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16 Q8PGK5
5 Q9332
6 Q8HZY3
10 Q94JH4
11 Q94JH3
10 Q94H28
3 Q08693
11 Q8C872
11 Q8C872
9 Q08919
6 Q8PF58
6 Q8PF58
6 Q8PF58
6 Q8PF58
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              Q9hba9 homo sapien Q8tay3 homo sapien Q8tay3 homo sapien Q8gyk5 xanthomonas Q93332 caenorhabdi Q8hzv3 sus scrofa Q94jh4 oryza sativ Q8lq61 oryza sativ Q9xh28 arabidopsis Q08693 saccharomyc Q8c872 mus musculu Q08919 saccharomyc Q9pf58 xylella fas Q8p530 xanthomonas Q8p530 xanthomonas Q9a5a8 caulobacter
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     Q8pps0 xanthomonas
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45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17
117	120	120	120.5	121	121.5	122.5	122.5	122.5	126	126.5	128.5	130.5	131	131	133	133.5	136	137.5	138	139.5	142.5	144.5	•	146.5	148	149	151	152.5
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Q8vus4 alteromonas	Q8pef6 xanthomonas		Q9f2x2 streptomyce	Q8prd7 xanthomonas	8 pse	homo			Q53737 streptomyce	a		P96264 mycobacteri	Q9zlyl rattus norv	0	Q04033 saccharomyc	Q8pfh7 xanthomonas		Q8ty04 methanopyru	Q8ck35 streptomyce	082996 aeromonas p	Q8phe8 xanthomonas	Q93ej5 bacillus li	Q8p3z6 xanthomonas	Q8p625 xanthomonas	Q9kld3 vibrio chol	P96152 vibrio chol	-	Q9a3u5 caulobacter

ALIGNMENTS

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Query Match Best Local Similarity Matches 442; Conser	Q9HBA9 Q9HBA9 Q9HBA9; Q1-MAR-2001 (TIEMBLEE Q1-MAR-2001 (TIEMBLEE Q1-MAR-2001 (TIEMBLEE Q1-MAR-2003 (TIEMBLEE Q1-MAR-2003 (TIEMBLEE PROSTATE-SPECIFIC MEN PSMAL/GCP III HOMO SAPIENS (HUMBAN). EUKATYOTA; METAZOA; C MAMMALIA; EUTHOTIA; F NCBI_TAXID=9606; [1] TISSUE=LIVEF; O'Keefe D.S., Bacich "EXPTESSION PROFILE C VERSUS A PROSTATE-SPE TISSUE=LIVEF; O'Keefe D.S., Bacich "Cloning and Characte peptidase that maps t Schizophrenia?"; SUBMLITED (APR-2000) EMBL; AFAG1715, AAG29 Pfam; PF04253; TFR_di SPGUENCE 442 AA; 5
tch 100.0%; al Similarity 100.0%; 442; Conservative 0;	IMINARY; MBLrel. 16, C MBLrel. 23, L C membrane an man). cich D.J., He cich D.J., He ile of Prosta e-Specific Me e-Cancer and 000) to the E A. A. A. Cich D.J., He cich D.J
Score 2329; Pred. No. 1. Mismatches	PRT; 4 Created) Last seque Last annot ntigen-lik ; Craniata;; Craniata;; Catarrhi ; Catarrhi funor Ass EMBL/GenBa c. 26CD6E0
DB 4; 6e-170; 0;	PRT; 442 AA. Created) Last sequence update) Last sequence update) Intigen-like protein. Craniata; Vertebrata; Eutele; Catarrhini; Hominidae; Homo. Catarrhini; Hominidae; Homo. Tumor Associated Vasculature. EMBL/GenBank/DDBJ databases. eston W.D.W.; leston W.D.W.; mof a novel glutamate-preferroczDII locus: a candidate gene EMBL/GenBank/DDBJ databases. 26CD6E082AC1E8D3 CRC64;
Length 442; Indels C	e) ate) ata; Euteleostomi; idae; Homo. idae; Homo. pswa) e Gene in Normal asculature."; atabases. atabases. crc64;
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Best Local
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InterPro; IPR003137; PA.
Pfam; PF02225; PA; 1
Pfam; PF04253; TFR_dimer; 1.
PROSITE; PS50840; PA; 1.
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01-JUN-2002
01-MAR-2003
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Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                             Local Similarity
    429
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                                                                                                                                                                                                               1 MGGSAPPDSSWRGSLKVSYNVGPGFTGNFSTQKVKMHIHSTNEVTRIYNVIGTLRGAVEP
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                                                                                                                    DRYVILGGHRDSWVFGGIDPQSGAAVVHETVRSFGTLKKEGWRPRRTILFASWDAEEFGL
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MGGSAPPDSSWRGSLKVPYNVGPGFTGNFSTQKVKMHIHSTNEVTRIYNVIGTLRGAVEP
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Primates;
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Last annotation updat
                                                                                                                                                                                                                                                                                     6;
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                                                                                                                                                                                                                                                                                                           Score 2097.5;
Pred. No. 1.9
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                                                                                                                                                                                                                                                                                                                                                                                   AF79A10CA2BF9DF4 CRC64;
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Q8PGK5;
01-OCT-2002
01-OCT-2002
01-MAR-2003
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XAC3611.
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Camarotte G., Cannavan F., Cardozo J., Chambergo F., Ciapina L.P., Cicarelii R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorry H., Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T., Formighiteri E.F., Franco M.C., Greggio C.C., Gruber A., Katsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F., Locali E.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M., Martins E.C., Meidanis J., Menck C.F.M., Miyaki C.Y., Moon D.H., Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R., Moreira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F., Spinola L.A.F., Takita M.A., Tamura R.E., Teixeira E.C., Tezza R.I.D., Tindade dos Santos M., Truffi D., Tsai S.M., White F.F., Setubal J.C., Kitajima J.P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=306 / ATCC 13902 / XV 101;

MEDLINE=22022145; PubMed=12024217;

da Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R.,

Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,

Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.E.A.,
                                                                                                                                                                                                                                                                                                                           Nature 417:459-463(2002).
EMBL; AE012011; AAM38454.1;
Pfam; PF04253; TFR_dimer; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Xanthomonadaceae;
NCBI_TaxID=92829;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Xanthomonas axonopodis (pv. citri).
Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
                                                                                                                                                                                                                                                                                                       Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                       "Comparison of the genomes of two Xanthomonas pathogens with host specificities.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                 Similarity
                           EPDRYVILGGHRDSWVFGGIDPOSGAAVVHETVRSFGTLKKEGWRPRRTILFASWDAEEF
YPDQWVVRGNHRDGWVFGAADPLSGTTALLAEAKAIGELAKQGQRPKRTLVYASWDGEEA
                                                                                             LGGPVAPE-DWRGALPITYRIG------GDAKARVHLKVDADWGSQTIYNVIATLRGSE
                                                                                                                                         MGGSAPPDSSWRGSLKVSYNVGPGFTGNFSTQKVKMHIHSTNE--VTRIYNVIGTLRGAV 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KRQISVAAFTVQAAAETLSEVA 442
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(TrEMBLrel.
(TrEMBLrel.
                                                                                                                                                                                           Conservative
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                                                                                                                                                                                           78;
                                                                                                                                                                                 Score 571.5; DB 10, Pred. No. 2.3e-35;
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Last annotation updat
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                                                                                                                                       Query Match
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WOrmPep; C35C5.2; CE08584.
InterPro; IPRO03137; PA.
Pfam; PF02225; PA; 2.
Pfam; PF04253; TFR_dimer; 2.
PROSITE; PS50840; PA; 2.
                                                                                                                                                                    PROSITE;
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Nemato
Rhabditidae; Peloderinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-FEB-1997 (TrEMBLrel.
01-FEB-1997 (TrEMBLrel.
01-MAR-2003 (TrEMBLrel.
                                                                                                                                                                                                                                                               investigating biology.";
Science 282:2012-2018(1998).
EMBL; 278417; CAB01688.1; -.
                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE=99069613; PubMed=9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Caenorhabditis elegans.
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                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                        "Genome sequence of the nematode C.elegans:
                                                                                                                           Local
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                                                                                                            al Similarity
147; Conserv
                           45
                                                                                                                                                                    PS50840; P.
1483 AA;
RKIQNIMGYIKGSQEPDKFVLVSNHYDAWTYGAVDPNSGTSTLLEVSRALKQYQNQTGWI
                 TRIYNVIGTLRGAVEPDRYVILGGHRDSWVFGGIDPQSGAAVVHETVRSFGTLKKE-GWR
                                                       MKGDA-VNADFQGKLNVTYRYGPGLINN----QKLRVTVHAENEERSVIVVELISRLRLNF
                                                                             MGGSAPPDSSWRGSLKVSYNVGPGFTGNFSTQKVKMHIHSTNE----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VQTAA 596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VQAAA 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KAAVPQIDFAALDQAIT-RLQDSAKRYDMALAARGGNLDAHVRSKLNASLQRIDQTLLAE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GFE----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GLLGSTEWAEDNSRLLQERGVAYINADSSIEGNYTLRVDCTPLMYSLVYNLTKELKSPDE 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LGLPDRPFYRHVIYAPSSHNKYAGESFPGIYDALFDIESKVDPSKAWGDVKRQISVAAFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LATLDLGY-----GGQGGGSGVYHSLYDSYDYFARFIDPQFAYLPLLSQTVGRTVLRVAN
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                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -FTEIASKFSERLQDFDKSNPILL------RMMNDQLMFLERAFIDP
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                                                                                                                          23.4%;
31.1%;
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23,
                                                                                                                                                                                                                                                                                                                                                                              the EMBL/GenBank/DDBJ
                                                                                                              84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Last sequence up
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Created)
                                                                                                           Score 545.5; DB 5;
Pred. No. 8.5e-33;
4; Mismatches 181;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GKSLYESWTKKSPSPEFSGMPRISKLGSGNDFEVFFQRLG
                                                                                                                                                                    AE07537AD85E8FFC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1483
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                                                                                                                                                                                                                                                                                                         platform
                                                                                                                                                                                                                                                                                                                                                                               databases
                                                                                                                                       Length 1483;
                                                                                                           Indels
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Q8HZV3
              멍
                                  QY
                                                                    밁
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                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 112; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q8HZV3;
Q8HZV3;
Q1-MAR-2003
                                                                                                                                                                                                                                                                                                                                                  Receptor.
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                           Python P., Jorg H., Neuenschwander S., Stranzinger G., Voge: "The complete cDNA sequence of porcine transferrin receptor Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.

EMBL; AF416763; AAN09749.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sus scrofa (Pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Transferrin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAR-2003
01-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                  rissue=small intestine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9823;
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                                                                    534
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              563
                                       237
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                659
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                                                                                                                                                                                                                                       364
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                                                                                                                                                                                               RDSWVFGGIDPQSGAAVVHETVRSFGTLKKEG-WRPRRTILFASWDAEEFGLLGSTEWAE
                                                                                                                                                                                                                                     TWRTDFPCKLVSSP-----SKNVKLTVNNVLKEIKILNIFGVIKGFEEPDRYVIVGAQ 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VIYAPSSHNKYAGESFPGIYDALFDIESKVDPSKAWGDVKRQISVAAFTVQAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QFKLLQKTVLELSEIVQRRNVSKLEELPFGSRVDINNRLIEFEKCFINPHGAIGNPQARH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SLVYNLTKELKSPD--EGFEG-KSLYESWTKKSPSPEFSGMPRISKL-GSGNDFEVFFQR 219 ::: : |: | :| |: | ||
                                    KF-----SGYPLYHSVYETYELVEKFYDPMFKYHLTVAQVRGGMVFELANSIVLPFDCRD 291
                                                                                            ESWTKK-----SPSPEFSGMPRISKLGSGNDFEVFFQRLGIASGRARYTKNWETN 236
                                                                                                                                                    DNSRLLQERGVAYINADSSIEGNYTLRVDCTPLMYSLVYNLTKELKSPDEGFEGKSLY--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGMVFELANSIVLPFDCRDYAVVLRKYADKIYNISMKHPQEM-KTYSL--SFDSLFSAVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LGIPIVFFITSSLDAPPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NVLRSAAANVEQPNPTEMEQGRKTLYDSWKYYAPSKNNRSTHPYQRIPAGGSDHLPFFDY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PARSILFAHWDAEEYGLIGSTEFAEEYRLQLMRRAVAVINMD-LIGGNQTLLGLSNPTVA
             -FCFCEDTDYPYLGTTMDTYDVLSKRVPQLNRMARAAAEVAGHLVIKLTIDFELNLN---
                                                                                                                        GYLSSLHLKAFTYINLDKAVLGTSNFKVSASPLLYSLIEKMMQDVKNP---VTGQSLYRD
                                                                                                                                                                               RDAWGPGAAKSSVGTSLLLNLAQILSDMVIKGQFKPSRSIVFASWSAGDFGAIGATEWLE
                                                                                                                                                                                                                                                               SWRGSLKVSYNVGPGFTGNFSTQKVKMHIHSTNEVTRIYNVIGTLRGAVEPDRYVILGGH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VLFHPSPDNWYDGDAISQVHDLISKISNSTD-SKELGKLSRQLAKEIALVNVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NFTEIASKFSERLQDFDKSN------PILLRM-MNDQLMFLERAFIDPLGLPDRPFYRH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IECILKFTESKILPYDLNEL-----MDDSIFEYLPKLEDRLNKTLMIGTKTDYLLDAQK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LGI-----ASGRARYTKNWETNKFSGYPLYHSVYETYELVEKFYDPMFKYHLTVAQVR 272
                                                                                                                                                                                                                                                                                                                                                  768 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Grembirel.
Grembirel.
Grembirel.
                                                                                                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                                                                                                                  86121 MW;
                                                                                                                                                                                                                                                                                                        17.8%;
24.7%;
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23, Last sequ
23, Last anno
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                                                                                                                                                                                                                                                                                        Score 415.5; DB 6;
Pred. No. 3.1e-23;
0; Mismatches 169;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                  55B15CEFA2F4D1CF CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      768
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Sus

Vogeli

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768; 83;

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Euteleostomi;

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ID 094J
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q94JH4;
01-DEC-2001
01-DEC-2001
01-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sasaki T., Matsumoto T., Yamamoto K.;
"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1,
clone:P063BD12:";
Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AP002972; BAB55507.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF02325; PA; 1.
Pfam; PF04253; TFR_dimer; 1.
PROSITE; PS50840; PA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-CV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Viridiplantae; Stro
Spermatophyta; Magnoliophyta;
Ehrhartoideae; Oryzeae; Oryza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Oryza sativa (Rice).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Peptidase-like protein. P0638D12.15.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=4530;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR003137; PA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                        415
        521
                                                          347
                                                                                                               470
                                                                                                                                                                                                                                                                                                                              423
                                                                                                                                                                                                                         459
                                                                                                                                                                                                                                                                            232
                                                                                                                                                                                                                                                                                                                                                                                   173
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          355 VIEGAEEPDRYVILGNHRDAWTFGASDPNSGTAAMIELAQRLSVLQKQGWRPRRTIIFCS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MGGSAPPDSSWRG-SLKVSYNVGPG-----FTGNFSTQKVKMHIHSTNEVTRIYNVIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WDAEEFGLLGSTEWAEDNSRLLQERGVAYINADSSIEGNYTLRVDCTPLMYSLVYNLTKE 172
SSNQLKKDSMKIRSLNDRLMQAERAFTNREGLFKREWFKHLVYGPSEQNDWESASYPGVE
                                                                                                                                                         RDYAVVLRKYADKIYNISMKHPQEMKTYSLSFDSLFSAVKNFTEIASKFSERLQDFD---
                                                                                                                                                                                                                       SCGWRNSEIQG-----
                                                                                                                                                                                                                                                                                                                           VQDPDN--SSQAVYDSWVKSNISPLDQAIPYI------
                                                                                                                                                                                                                                                                                                                                                                             LKSPDEGFEGKSLYESWTKKSPSPEFSGMPRISKLGSGNDFEVFFQRLGIASGRARYTK- 231
                                                                                                                                                                                                                                                                                                                                                                                                                                           WDAEEYGL - - -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LGGDAAP-ADWQGREGSPYYRLGPGPAILNLTYTGN-------DTMATIENVFA 354
                                                  ----KSNPILLRMMNDQLMFLERAFIDPLGLPDRPFYRHVIYAPSSHNKYAGESFPGIY 401
                                                                                                       --SVGTLQAYTKVVEN-----EVRGTAISCSPLHNAIRALKTAATKVNGERKELQRQL
                                                                                                                                                                                                                                                                      -- NWETNKFSGYPLYHSVYETYELVEKFYDPMFKYHLTVAQVRGGMVFELANSIVLPFDC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KLRQKNSSAFNQTLLKNQLALATWTIQGAANALS 758
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ESKVDPSKAWGD--VKRQISVAAFTVQAAAETLS 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DKFVMREINDRIMKVEYHFLSPYVSPRESPFRHIFWGSGSHT-----LSALVEHL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----YEMYNDKILSFVREMNQFRVDIREMGLSLQWLYSARGDFFRATSRLTSDYRNVETR 674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YAVVLRKYADKIYNISMKHPQ---EMKTYSLSFDSLFSAVKNFTEIASKFSERLQDFDKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nipponbare;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        621 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17.78;
24.28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     67139 MW; 8D471DA2259016A4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19,
19,
23,
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yta; Liliopsida; Poales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63; Mismatches 116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Last sequence up
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 412; DB 10;
Pred. No. 4.2e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Embryophyta; Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8
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RESULT 8
Q94JH3
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Best Local Sim
Matches 101;
                                                                                                                                                                           Q94JH3
Q94JH3;
Q94JH3;
01-DEC-2001 (TrEMBLrel. 1
01-DEC-2001 (TrEMBLrel. 1
01-MAR-2003 (TrEMBLrel. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            O8LO61; PRELIMINARY; O8LO61; O1-OCT-2002 (TremBLrel. 201-OCT-2002 (TremBLrel. 201-OCT-2003 (TremBLrel. 201-MAR-2003 (TremBLrel. 201-MAR-201-MAR-2003 (TremBLrel. 201-MAR-2003 (TremBLrel. 201-MAR-20
Oryza sativa (Rice).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                           Peptidase-like protein. P0638D12.16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Oryza sativa (japonica cultivar-group).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
NCBI_TaxID=39947;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases EMBL; AP003768; BAB91937.1; -. Gramene; Q8LQ61; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Putative peptidase-like protein. P0439E07.19.
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Sasaki T., Matsumoto T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         300 ADKIYNISMKHP------QEMKTYSLSFDSLFSAVKNFTEIASKFSERLQDFDKSN 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  108 EYAVYHSLYDDFVWMEKFGDPLFRRHVAAASMWGLVALRLSDEEILPFNYSTYAVELEKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     240 GYPLYHSVYETYELVEKFYDPMFKYHLTVAQVRGGMVFELANSIVLPFDCRDYAVVLRKY
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(TrEMBLrel. 22, Last sequence update)
(TrEMBLrel. 23, Last annotation update)
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Last sequence update)
Last annotation updat
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RESULT 9
QXX12B
ID QXX1B
ID QXXB
ID QXXB
AC Q9XH
AC Q9XH
DT 01-N
DT 01
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Matches 100;
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                                                                                                                                                                       Q9XH28;
Q9XH28;
Ol-NOV-1999 (TrEMBLrel. 12, Created)
Ol-NOV-1999 (TrEMBLrel. 12, Last sequence update)
Ol-NOV-1999 (TrEMBLrel. 23, Last annotation update)
Ol-MAR-2003 (TrEMBLrel. 23, Last annotation update)
F10A2.10 protein (Putative peptidase).
F10A2.10 OR A74GO7670.
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
"The A. thaliana Genome Sequencing Project."; Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases
                                                                                  STRAIN-CV.
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Pfam; PF04253; TFR_dimer; 1.
PROSITE; PS50840; PA; 1.
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                                                             WASHU;
                                                                               SEQUENCE FROM N.A.
STRAIN-CV. Columbia;
                                                                                                                                                          NCBI_TaxID=3702;
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22.4%; Pred. No. 1.
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RESULT 10
Q08693
ID 00869
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Submitted (MAR-2000) to the E
EMBL; AR147259; AAD29787.1; -
EMBL; AL161506; CAB81137.1; -
HSSP; PD2786; 1CX8.
InterPro; IPR003137; PA.
Pfam; PF02225; PA; 1.
MEDLINE-97298311; PubMed-9153759;
Jauniaux J.C., Poirey R.;
"Sequencing analysis of a 36.8 kb fragment of yeast chromosome reveals 26 open reading frames including SEC63, CDC31, SUG2, GC RBL2, PNT1, PAC1 and VPH1.";
Yeast 13:483-487(1997).
EMBL; Z75164; CAA99478.1; -.
SGD; S0005782; YOR256C.
                                                                                                                                                                                                                                                                                         Q08693;
Q08693;
                                                                                                                                                                                                                                     01-NOV-1996 (TrEMBLrel. 01, 01-NOV-1996 (TrEMBLrel. 01, 01-MAR-2003 (TrEMBLrel. 23, Chromosome XV reading frame
                                                                                                                                                                          Eukaryota; Fungi; Ascomycota; Saccharomycotina; Sacc
Saccharomycetales; Saccharomycetaceae; Saccharomyces
NCBI_TaxID=4932;
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Joshu C., Bauer C., Hotic M.;
"The sequence of A. thaliana F10A2.";
Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                  SEQUENCE FROM N.A.
                                                                                                                           Submitted (JUL-1996) to
                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                Saccharomyces cerevisiae (Baker's yeast)
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5; PS50840; PA; 1.
790 AA; 31115 MW;
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Last annotation updat
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pfam; PF02225; PA; 1.
pfam; PF04253; TFR_dimer; 1.
pR0SITE; PS50840; PA; 1.
SEQUENCE 809 AA; 91995 MW;
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01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last seq
01-MAR-2003 (TrEMBLrel. 23, Last ann
Transferrin receptor.
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STRAIN-C57BL/6J; TISSUE-Head;
MEDLINE-22354683; PubMed-12466851;
                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                          the RIKEN Genome Exploration Research Group "Analysis of the mouse transcriptome based o 60,770 full-length cDNAs.";
Nature 420:563-573(2002).
EMBL; AK046728; BAC33277.1; -.
ESQUENCE 515 AA; 57341 MW; 86FC77FF66A80
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MGGSAPP----DSSWRGSLKVSYNVGPGFTGNFSTQKVKMHIHSTNEVTRIYNVIGTLRG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 240.5; DB 3;
Pred. No. 9.2e-10;
B; Mismatches 160;
                                                                                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation updat
                                                        Score 224.5; DB Pred. No. 8e-09; 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             D7D68C0A8C50ECB2 CRC64;
                                                                                                                                                                                                                                                                                                                                                  Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                 86FC77FF66A80DDF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   515
                                                                                                                                                                                                       p Phase I & II
on functional
                                                                                              DB 11;
                                                                                                                                                                                                                                                                                                                                                                                                                           update)
                                                            52;
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                                                              Indels
                                                                                              Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; 608
                                                                                                                                                                                                            annotation
                                                                                                                                                                                                                            Team;
                                                                                                   515;
                                                              21;
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Best Local S
Matches 93
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Q08919;
Q1-NOV-1996
Q1-NOV-1996
Q1-NOV-1996
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Chromosome XVI reading frame ORF YPL176C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetales; Saccharomycetaceae; Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (MAY-1996) to the EMBL; 273532; CAA97883.1; -. SGD; S0006097; YPL176C. InterPro; IPR003137; PA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF02225; PA; 1.
Pfam; PF04253; TFR_dimer; 1.
PROSITE; PS50840; PA; 1.
SEQUENCE 783 AA; 88755 MW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          114 DAEEFGLLGSTEWAEDNSRLLQERGVAYINADSSIEGNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             374 VKFSNNL---FSGSLNDCRLDLLVQTAIRERHPVHDIVGKIEGSEQAGRAIVIAAPRNSA 430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       74 VFGGIDPQSGAAVVHETVRSFGTL-KKEGWRPRRTILFASWDAEEFGLLGSTEWAEDNSR 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15 LKVSYNVGPGFTGNFSTQKVKMHIHST-NEVTRIYNVIGTLRGAVEPDRYVILGGHRDSW 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YEEPDDRYVVVGAQRDA-LGAGVAAKSSVGTGLLLKLAQVFSDMISKDGFRPSRSIIFASW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AVEPDRYVILGGHRDSWVFGGIDPQS--GAAVVHETVRSFG-TLKKEGWRPRRTILFASW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEGSCPARWNIDSSCK--LELSQN---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                  SYGTMYPSFGTVVLLSLIQLYQEMVYKFDWKPLRNIYFISFGGSEFNEAGATELMEKRTE
                                                                                                                                                                                                                                   FSGYPLYHSVYETYELVEKFYDPMFKYHLTVAQVRGGMVFELANSIVLPFDCRDYAVVLR
                                                                                                                                                                                                                                                                             HQFGDWT----PYLAQGIPVAIISSPGVMNREHPIYTVEDKFDFIKDKLRDKKKGEV--
                                                                                                                                                                                                                                                                                                              YE--SWTKKSPSPEFS-GMP--RISKLGSGNDFEVFF---QRLGIASGRARYTKNWETNK
                                                                                                                                                                                                                                                                                                                                                        ALKSEIYTIIDVGQIGIWDDSN----NLEIQCHPLLVDL---FQKNMTSRKFNVKVDNV
                                                                                                                                                                                                                                                                                                                                                                              LLQERGVAYINA------DSSIEGNYTLRVDCTPLMYSLVYNLTKELKSPDEGFEGKSL 185
                                                                                                                                                         KYADKIYNISMKHPQEMKTYSLSFDSLFSAVKNFTEIASKFSERLQDFDKSNPILLRMMN
                                                                                                                                                                                               LSEIMLY-----LVEK-------SLELIDDPFIPFSISNYVDFL-
GESFPGIYDALFDIESKVDPSKAW--GDVKRQISVAAF-TVQAAAETLSEV
                                        TELMYGAGTY1EPTIIAINRWSWNYLLSLIGVTQCLEEGLMDRTFYKNVIFGPKLW----
                                                                                DQLMFLERAFIDPL----
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                                                                                                                    -STTLKDLQKECPDTVNFDEVFLGTTLWENTKLQFEKWKSEW-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          88755 MW;
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the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 179.5; DB 3
Pred. No. 4.2e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches 169;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          85D78D5D2FE114A7
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J databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    152
                                                                                      -GLPDRPFYRHVIYAPSSHNKYA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                495
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                441
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RA Alvarenga R., Alves L.M.C., Araya J.E., Baia G.S., Baptista C.S.,
RA Alvarenga R., Alves L.M.C., Araya J.E., Baia G.S., Baptista C.S.,
RA Alvarenga R., Alves L.M.C., Araya J.E., Baia G.S., Baptista C.S.,
RA Alvarenga R., Alves L.M.C., Araya J.E., Bave J.M., Briones M.R.S.,
RA Barros M.H., Bonaccorsi E.D., Bordin S., Bove J.M., Briones M.R.S.,
RA Bueno M.R.P., Camargo A.A., Camargo L.E.A., Carraro D.M., Carrer H.,
RA Colauto N.B., Colombo C., Costa F.F., Costa M.C.R., Costa-Neto C.M.,
RA Colauto N.B., Colombo C., Costa F.F., Costa M.C.R., Cerrer H.,
RA Colauto N.B., Colombo C., Costa F.F., Costa M.C.R., Ell-Dorry H.,
RA Colauto N.B., Colombo C., Costa M.C., Frohme M., Furlan L.R.,
RA Garnier M., Goldman G.H., Goldman M.H.S., Gomes S.L., Kitajina J.P.,
RA Garnier M., Goldman G.H., Goldman M.H.S., Gomes S.L., Kitajina J.P.,
RA Kiteger J.E., Kuramae E.E., Laigret F., Lambais M.R., Leite L.C.C.,
RA Lemos E.G.M., Lemos M.V.F., Lopes S.A., Lopes C.R., Machado J.A.,
RA Lemos E.G.M., Lemos M.V.F., Lopes S.A., Lopes C.R., Machado J.A.,
RA Macques M.V., Martins E.A.L., Martins E.M.F., Matsukuma A.Y.,
RA Mandado M.A., Nascimento A.L.T.O., Netto L.E.S.,
RA Menck C.F.M., Miracca E.C., Miyaki C.Y., Monteiro-vitorello C.B.,
RA Menck C.F.M., Miracca E.C., Miyaki C.Y., Monteiro-vitorello C.B.,
RA Menck C.F.M., Miracca E.G., Nunes L.R., Oliveira M.A.,
RA Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,
RA Menck C.F., Sereira G.A.G., Pereira H.A. Jr., Pesquero J.B.,
RA de Solva M.C., de Silva A.M., da Silva F.R., Silva W.A. Jr.,
RA de Solva A.C.R., da Silva A.M., da Silva F.R., Silva W.A. Jr.,
RA de Solva A.P., Terenzi M.F., Truffi D., Tsai S.M., Tsuhako M.H.,
RA Cagon M.A., Zatz M., Meidanis J., Setubal J.C.;
RT "The George Control of the nilant pathogen Xviella fastidiosa ".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 13
                                                                                                                                                                                                                                                                                                                          Query Match
Best Local
                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                    Hypothetical protein; Corstating SeQUENCE 520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "The genome sequence of the plant pathogen xylella fastidiosa."; Nature 406:151-159(2000).
EMBL; AE003921; AAF83630.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-OCT-2000 (TrEMBLrel. 15, 01-OCT-2000 (TrEMBLrel. 15, 01-MAR-2003 (TrEMBLrel. 23,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=20365717;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Xanthomonadaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Xylella fastidiosa.
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                                                                                                                                                                                                                                                          42
                                                                                                                                                                                                                                                                                                    66;
                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                    TVRSFGTLKKEGWRPRRTILFASWDAEEFGLLGSTEWAEDNSRLLQERGVAYINAD----
PEFSGMPRISKLGSGNDFEVFFQRLGIASGRA
                                            QGPTRDFGIYGTAKLDLLDMLKQVAAGWKLRYTLD----PTPEAGHFFRSDHFSFAKR---
                                                                                  ---SSIEGNY-TLRVDCTPLM-----YSLVYNLTKELKSPDEGFEGKSLYESWTKKSPS 195
                                                                                                                         LARGEA----RGPQPQRSVLFLAVTAEEKGLLGS-EYYASNPLYPLEKTVAVINMDVMNP
                                                                                                                                                                                                                                                          NEVTRIYNVIGTLRGAVEPDRYVILGGHRD-----SWVF-GGIDPQSGAAVVHE
                                                                                                                                                                                                              SEVITSHNVAARLQGCAHPDETVIYSAHWDHLGVGAPDAKGDTIFNGALDNASGTAALLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                    IPR000010; Cystatin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (TrEMBLrel.
                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein Xf0820
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PubMed=10910347;
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                                                                                                                                                                                                                                                                                                                                                                                        57664 MW;
                                                                                                                                                                                                                                                                                                                    7.48;
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                                                                                                                                                                                                                                                                                                                                                                             Complete proteome.
7664 MW; 37EFC71953B41655 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gammaproteobacteria; Xanthomonadales;
                                                                                                                                                                                                                                                                                                    30;
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Last annotation update)
                                                                                                                                                                                                                                                                                                                      Score 173; DB 16;
Pred. No. 7.5e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Created)
                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   529
                                                                                                                                                                                                                                                                                                    70;
                                                                                                                                                                                                                                                                                                                                        Length 529;
                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                  46;
                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                          89
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RESULT : Q8P530 OR Q8P530 OR AC Q8P530 OR AC
  RESULT 15
Q9A5A8
ID Q9A5A
AC Q9A5A
DT 01-JU
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DT 01-JU
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local S
Matches 59
                                                                 Q9A5A8;
Q9A5A8;
Q1-JUN-2001
01-JUN-2001
01-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q8P530;
01-OCT-2002
Caulobacter crescentus
                                            Aminopeptidase, putative.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AE012471; AAM42787.1; -. Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Trindade dos Santos M., Truf
Setubal J.C., Kitajima J.P.,
"Comparison of the genomes o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Xanthomonas campestris (pv. campestris).
Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q8P530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       host specificities.";
Nature 417:459-463(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Xanthomonadaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    351 LARGFA----KGPKPERSVVFLAVTAEEKGLLGSEFYA---SKPLYPLATTVAVINMDGM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          291 SDVITSHNVVARLEGSTHPDETLIYSAHWDHIGVGKPDARGDTIFNGALDNASGTAALLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            90 TVRSFGTLKKEGWRPRRTILFASWDAEEFGLLGSTEWAEDNSRLLQERG--VAYINAD--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    42 NEVTRIYNVIGTLRGAVEPDRYVILGGH------RDSWVF-GGIDPQSGAAVVHE 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                KSLYESWTKKSPSPEFSGMPRISKLGSGNDFEVFFQRLGIASGRA
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                                                                 (TrEMBLrel. 17,
(TrEMBLrel. 17,
(TrEMBLrel. 23,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6.8%;
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                                                                                                                                                                                                                                                                      --GVPALS-YAAGQDWEVG---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               of two Xanthomonas pathogens with differing
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Last annotation update)
                                                                                                               Created)
                                                                   Last annotation update)
                                                                                          Last sequence update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 158; DB 16; Pred. No. 0.0011;
                                                                                                                                                           PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        B6FB8307A172C071 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
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                                                                                                                                                                                                                                                                      -GVAAGKA
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Search completed: October 4, 2003, 23:25:13 Job time : 81 secs
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                                                                                                                                                                                                                                                                                                                                          Query Match 6.7%; Score 157; DB 16; Length 467; Best Local Similarity 30.3%; Pred. No. 0.0011; Matches 44; Conservative 28; Mismatches 59; Indels 14; Gaps
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STRAIN-ATCC 19089 / CB15;

MEDLINE-21173698; PubMed-11259647;

MEDLINE-21173698; PubMed-11259647;

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                                                                                                                                                                                                                                                                                                                                                                                                                                  Complete proteome. SEQUENCE 467 AA; 48918 MW; 9984DE2A9D84F00F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Froteobacteria; Alphaproteobacteria; Caulobacterales; Caulobacteraceae; Caulobacter. NCBI_TaxID=155892;
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                                                                            347 -ESDTGADRIYSLQVPAGSLDHPVV 370
                                                                                                                                142 INADSSIEGNYTLRVDCTPLMYSLV 166
                                                                                                                                                                    292 GTAITTAAAKLIGDLPK---RPKRTIRVVMWGSEESG--GSSEAYLAANKDALSTMVLAG 346
                                                                                                                                                                                                                                                            232 AARKVPMRVKLKLESSVNPNNVAWNISGDIKGSEKPDEVIVIGGHLDSWDVGTGALDDAT 291
                                                                                                                                                                                                                                                                                    83 GAAVVHETVRSFGTLKKEGWRPRRTILFASWDAEEFGLLGSTE-WAEDNSRLLQERGVAY 141
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